

Jarrell, Noble

181606

From: Ramirez, Delia
Sent: Tuesday, March 07, 2006 5:49 PM
To: Jarrell, Noble
Subject: 09/541,462

Hi,

I would like to request the following search:

1. an oligo search (at least 12 nucleotides long) of SEQ ID NO:1 and 2 in the nucleic acid databases (commercial only)

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

Noble

Fin 3/16/06

4 NA

oligo

20Pr

compugra

2000

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Jarrell, Noble

From: Ramirez, Delia
Sent: Tuesday, March 07, 2006 5:44 PM
To: Jarrell, Noble
Subject: 09/541,462

Hi,

I would like to request the following INTERFERENCE search:

1. SEQ ID NO:1 and 2 in the nucleic acid databases.
2. an oligo search (at least 12 nucleotides long) of SEQ ID NO:1 and 2 in the nucleic acid databases.

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2006, 09:47:22 ; Search time 530 Seconds
(without alignments)
470.166 Million cell updates/sec

Title: US-09-541-462B-2
Perfect score: 108
Sequence: 1 MAAMVDVTFSGTNSGAGKK.....KTRQVCPLDNREWFQYKH 108

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7673375 seqs, 115364844 residues
Word size: 12

Total number of hits satisfying chosen parameters: 12
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-DB=Published Applications_NA_New -QFMT=fastap -SURFIX=oligo.rnpbn
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=12
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abs06p
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-NO MMAP -NEG SCORES=0 -WAIT -BSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:

- 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	74	68.5	660	9	US-11-096-568A-11809 Sequence 11809, A
2	70	64.8	432	9	US-11-096-568A-14405 Sequence 14405, A
3	42	38.9	693	9	US-11-096-568A-26820 Sequence 26820, A
4	40	37.0	348	9	US-11-096-568A-28569 Sequence 28569, A

C	5	12	11.1	153	7	US-10-932-182A-81177	Sequence 81177, A
C	6	12	11.1	153	7	US-10-932-182A-81177	Sequence 81177, A
C	7	12	11.1	207	7	US-10-932-182A-6146	Sequence 6146, Ap
C	8	12	11.1	207	7	US-10-932-182A-6146	Sequence 6146, Ap
	9	12	11.1	366	7	US-10-932-182A-2279	Sequence 2279, Ap
	10	12	11.1	366	7	US-10-932-182A-2279	Sequence 2279, Ap
	11	12	11.1	366	7	US-10-932-182A-2279	Sequence 78459, A
	12	12	11.1	366	7	US-10-932-182A-78459	Sequence 78459, A

ALIGNMENTS

RESULT 1
US-11-096-568A-11809
; Sequence 11809, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11809
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(660)
; OTHER INFORMATION: Ceres Seq. ID no. 13657464
US-11-096-568A-11809

Alignment Scores:
Pred. No.: 1.49e-71 Length: 660
Score: 74.00 Matches: 74
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 68.5% Indels: 0
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x US-11-096-568A-11809 (1-660)

Qy	25	LVSLYSTPAsnAlaValAlaLeuTTPAlaTTPAspIleValValAspAsnCysAlaThr 44
Db	208	AGAAGTGGAAACGCCGCTCTGGCGTGGGACATCGTGGTGGACAACTGGCCCATC 267
Qy	45	CysArgAsnHisIleMetAppLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr 64
Db	268	TGCCGTAAACCATCATGATGATTTATGATCGAGTCCAGCCCAACGAGCCGCCACC 327
Qy	65	SerGluCysThrValAlaTTPGlyValCysAsnHisAlaPheHisCysIle 84
Db	328	AGCGAGGAGTGCACCGTCGCATCGGCTGTCTGTAAATCATGCTTCCACTCCACTGCATC 387
Qy	85	SerArgTTPLeuIysThrArgGlnValCysProLeuAspAsn 98
Db	388	AGCAGGTGGCTCAAGACTCGCCCAAGTGTGCCACTAGACAAC 429

RESULT 2

US-11-096-568A-14405
; Sequence 14405, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14405

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; LENGTH: 432
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(432)
; OTHER INFORMATION: Ceres Seq. ID no. 4776740
US-11-096-568A-14405

Alignment Scores:
Pred. No.: 2,64e-67 Length: 432
Score: 70.00 Matches: 70
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 64.8% Indels: 0
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x US-11-096-568A-14405 (1-432)

Qy 29 AlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHis 48
Db 188 GCGTGGCTCTCTGGGCTTGGGATATCGTTGGTACAAATTCGCGCATCTGCAGAAACAC 247
Qy 49 IleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCys 68
Db 248 ATCATGGATCTCTGATTGAATGTCAGGCTAATCAGCCAGCGCTACGAGTGAGGAATGC 307
Qy 69 ThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeu 88
Db 308 ACTGTTGCTTGGGGGGTTCGAATCAGCCCTTCACCTTCCTGCTGCATCAGCAGATGTTA 367
Qy 89 LysThrArgGlnValCysProLeuAspAsn 98
Db 368 AAGACTCGTCAAGTTGCCCATTCGATAAC 397

RESULT 3
US-11-096-568A-26820
; Sequence 26820, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26820
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(693)
; OTHER INFORMATION: Ceres Seq. ID no. 13622871
US-11-096-568A-26820

Alignment Scores:
Pred. No.: 2,29e-36 Length: 693
Score: 42.00 Matches: 42
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 38.9% Indels: 0
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x US-11-096-568A-26820 (1-693)

Qy 32 LeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAsp 51
Db 207 CTCTGGGCTGGACATCGTGGTGGACAACTGCGCCATCTGCCGCAACCATCATGAGAC 266
Qy 52 LeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAla 71
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Db 267 CTTTGCATCGAGTGCAGCGCAACCAAGCGAGCGCCACCGAGGAGTGACCGGTGCT 326
Qy 72 TrpGly 73
Db 327 TGGGGA 332

RESULT 4
US-11-096-568A-28569
; Sequence 28569, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28569
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(348)
; OTHER INFORMATION: Ceres Seq. ID no. 3017472
US-11-096-568A-28569

Alignment Scores:
Pred. No.: 2,07e-34 Length: 348
Score: 40.00 Matches: 68
Percent Similarity: 97.1% Conservative: 0
Best Local Similarity: 97.1% Mismatches: 1
Query Match: 37.0% Indels: 2
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x US-11-096-568A-28569 (1-348)

Qy 29 AlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHis 48
Db 106 GCTGTGCTCTCTGGGCTTGGGATATCGTTGGTAACTGCGCAATTTGTAGGAATCAC 165
Qy 49 IleMetAspLeuCysIleGluCysGln-AlaAsnGlnAlaSerAlaThrSerGluGluCys 68
Db 166 ATCATGGATCTCTGATTGAATGCT-AGCTAATCAGCTAGTCCACTAGTAGGAATG 224
Qy 68 sThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLe 88
Db 225 CACTGTTGCTTGGGGGGTTTGCACCAACCGCTTTCCTTCCTGCTATCAGCAGATGGCT 284
Qy 88 uLysThrArgGlnValCysProLeuAsp 97
Db 285 CAAAACTCGTCAAGTGTGCTCACTAGAT 312

RESULT 5
US-10-932-182A-81177/c
; Sequence 81177, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81177
; LENGTH: 153
; TYPE: DNA
```

ORGANISM: Saccharomyces pastorianus
US-10-932-182A-81177

Alignment Scores:
Pred. No.: 0.000629 Length: 153
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-81177 (1-153)

Qy 39 ValaspaenCysAlaIleCysArgAsnHisIleMet 50
Db 68 GTTGACAACTGTGCTATTTCAGGAACCATATAATG 33

RESULT 6

US-10-932-182A-81177/c
; Sequence 81177, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81177
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-81177

Alignment Scores:
Pred. No.: 0.000629 Length: 153
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-81177 (1-153)

Qy 39 ValaspaenCysAlaIleCysArgAsnHisIleMet 50
Db 68 GTTGACAACTGTGCTATTTCAGGAACCATATAATG 33

RESULT 7

US-10-932-182A-6146/c
; Sequence 6146, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6146
; LENGTH: 207
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-6146

US-10-932-182A-6146

Alignment Scores:
Pred. No.: 0.000804 Length: 207
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-6146 (1-207)

Qy 39 ValaspaenCysAlaIleCysArgAsnHisIleMet 50
Db 47 GTTGACAACTGTGCTATTTCAGGAACCATATAATG 12

RESULT 8

US-10-932-182A-6146/c
; Sequence 6146, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6146
; LENGTH: 207
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-6146

Alignment Scores:
Pred. No.: 0.000804 Length: 207
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-6146 (1-207)

Qy 39 ValaspaenCysAlaIleCysArgAsnHisIleMet 50
Db 47 GTTGACAACTGTGCTATTTCAGGAACCATATAATG 12

RESULT 9

US-10-932-182A-2279
; Sequence 2279, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2279
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2279

Alignment Scores:
 Pred. No.: 0.00128 Length: 366
 Score: 12.00 Matches: 12
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 11.1% Indels: 0
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
 |||||
 Db 154 GTTGACAACGTGCTATTTCAGAAACCATATG 189

RESULT 10

US-10-932-182A-78459
 ; Sequence 78459, Application US/10932182A
 ; Publication No. US20060046253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHISA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: 030685-043
 ; CURRENT APPLICATION NUMBER: US/10/932,182A
 ; CURRENT FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 78459
 ; LENGTH: 366
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 US-10-932-182A-78459

Alignment Scores:
 Pred. No.: 0.00128 Length: 366
 Score: 12.00 Matches: 12
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 11.1% Indels: 0
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-78459 (1-366)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
 |||||
 Db 154 GTTGACAACGTGCTATTTCAGAAACCATATG 189

RESULT 11

US-10-932-182A-2279
 ; Sequence 2279, Application US/10932182A
 ; Publication No. US20060046253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHISA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: 030685-043
 ; CURRENT APPLICATION NUMBER: US/10/932,182A
 ; CURRENT FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 2279
 ; LENGTH: 366
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 US-10-932-182A-2279

Alignment Scores:
 Pred. No.: 0.00128 Length: 366
 Score: 12.00 Matches: 12
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 11.1% Indels: 0
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
 |||||
 Db 154 GTTGACAACGTGCTATTTCAGAAACCATATG 189

RESULT 12

US-10-932-182A-78459
 ; Sequence 78459, Application US/10932182A
 ; Publication No. US20060046253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHISA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: 030685-043
 ; CURRENT APPLICATION NUMBER: US/10/932,182A
 ; CURRENT FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 78459
 ; LENGTH: 366
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 US-10-932-182A-78459

Alignment Scores:
 Pred. No.: 0.00128 Length: 366
 Score: 12.00 Matches: 12
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 11.1% Indels: 0
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-78459 (1-366)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
 |||||
 Db 154 GTTGACAACGTGCTATTTCAGAAACCATATG 189

Search completed: March 11, 2006, 12:07:37
 Job time : 531 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2006, 08:24:33 ; Search time 653 Seconds
(without alignments)
1367.677 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 616
Sequence: 1 MAAMVDVTPSGTSGAGKK.....KTRQVCLDNREWFQYKH 108

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abse/ABSSWEB_spool/US09541462/runat_10032006_080735_22137/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fasap -SUFFIX=rnpsbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abse05h
-USER=US09541462 @CGN_1_1026 @runat_10032006_080735_22137 -NCPUs=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	100.0	433	7	US-10-242-535A-43377
2	616	100.0	433	7	US-10-085-783A-43377
3	616	100.0	453	7	US-10-242-535A-35025
4	616	100.0	453	7	US-10-085-783A-35025
5	616	100.0	467	7	US-10-242-535A-39933
6	616	100.0	467	7	US-10-085-783A-39933
7	616	100.0	471	7	US-10-242-535A-57254

8	616	100.0	471	7	US-10-085-783A-57254
9	616	100.0	472	7	US-10-242-535A-56068
10	616	100.0	472	7	US-10-085-783A-56068
11	616	100.0	504	8	US-10-913-937-5
12	616	100.0	508	8	US-10-913-937-3
13	616	100.0	523	7	US-10-242-535A-46292
14	616	100.0	523	7	US-10-085-783A-46292
15	611	99.2	476	3	US-09-918-995-17191
16	607	98.5	4543	5	US-10-198-846-11311
17	603	97.9	430	7	US-10-242-535A-54751
18	603	97.9	430	7	US-10-085-783A-54751
19	596	96.8	380	3	US-09-960-352-4677
20	586	95.1	4476	8	US-10-357-930-25604
21	573	93.0	5347	6	US-10-240-965-99
22	554	89.9	3484	8	US-10-723-860-1383
23	554	89.9	3484	9	US-10-756-149-1357
24	554	89.9	5111	5	US-10-205-823-382
25	554	89.9	5111	10	US-11-051-454-382
26	554	89.9	5371	8	US-10-723-860-5852
27	545	88.5	468	7	US-10-242-535A-47656
28	545	88.5	468	7	US-10-085-783A-47656
29	535	86.9	692	10	US-11-097-143-31031
30	524	85.1	840	7	US-10-767-701-12172
31	523.5	85.0	527	9	US-10-487-901-4266
32	523.5	85.0	531	9	US-10-487-901-4271
33	523.5	85.0	586	9	US-10-487-901-4270
34	523.5	85.0	617	9	US-10-487-901-4265
35	523.5	85.0	691	9	US-10-487-901-4263
36	523.5	85.0	1259	7	US-10-437-963-11395
37	522.5	84.8	619	7	US-10-425-114-25647
38	521	84.6	683	9	US-10-487-901-4262
39	520	84.4	673	9	US-10-487-901-4261
40	519.5	84.3	553	7	US-10-021-323-10545
41	519.5	84.3	553	8	US-10-767-795-687
42	518.5	84.2	824	7	US-10-424-599-6074
43	515.5	83.7	390	3	US-08-770-791-20
44	515.5	83.7	893	8	US-10-425-115-16831
45	514.5	83.5	544	8	US-10-767-795-688

ALIGNMENTS

RESULT 1
US-10-242-535A-43377
; Sequence 43377, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43377
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-43377

Alignment Scores:
Pred. No.: 2.71e-74 Length: 433
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-43377 (1-433)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20
Db 20 ATGGCGCAGCGATGGATGGATACCCCGAGCGGCCAACACGCGCGGGCAAGAAG 79
Qy 21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 80 CGCTTTGAGAGTGAAGAGTGAATGAGTACCTCTGGCGCTGGGATATTTGGTTGAT 139
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysLysGluCysGlnAlaAsnGln 60
Db 140 AACGTGCGCATCTCGAGAACACCATATATGGATCTTTGCATAGAAATGCAAGCTAACCG 199
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 200 GCGTCCGCTACTTCCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 259
Qy 81 PheHisCysIleSerArgTyrLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 260 TTCACCTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGCAACAGAGAG 319
Qy 101 TrpGluPheGlnLysTyrGlyHis 108
Db 320 TGGGAATTCAAAAGATATGGGCAC 343

RESULT 2

US-10-085-783A-43377
; Sequence 43377, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43377
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human

US-10-085-783A-43377

Alignment Scores:
Pred. No.: 2,71e-74 Length: 433
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-43377 (1-433)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20
Db 20 ATGGCGCAGCGATGGATGGATACCCCGAGCGGCCAACACGCGCGGGCAAGAAG 79
Qy 21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 80 CGCTTTGAGAGTGAAGAGTGAATGAGTACCTCTGGCGCTGGGATATTTGGTTGAT 139

Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysLysGluCysGlnAlaAsnGln 60
Db 140 AACGTGCGCATCTCGAGAACACCATATATGGATCTTTGCATAGAAATGCAAGCTAACCG 199
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 200 GCGTCCGCTACTTCCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 259
Qy 81 PheHisCysIleSerArgTyrLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 260 TTCACCTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGCAACAGAGAG 319
Qy 101 TrpGluPheGlnLysTyrGlyHis 108
Db 320 TGGGAATTCAAAAGATATGGGCAC 343

RESULT 3

US-10-242-535A-35025
; Sequence 35025, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35025
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Human

US-10-242-535A-35025

Alignment Scores:
Pred. No.: 2,89e-74 Length: 453
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-35025 (1-453)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20
Db 24 ATGGCGCAGCGATGGATGGATACCCCGAGCGGCCAACACGCGCGGGCAAGAAG 83
Qy 21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 84 CGCTTTGAGAGTGAAGAGTGAATGAGTACCTCTGGCGCTGGGATATTTGGTTGAT 143
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysLysGluCysGlnAlaAsnGln 60
Db 144 AACGTGCGCATCTCGAGAACACCATATATGGATCTTTGCATAGAAATGCAAGCTAACCG 203
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 204 GCGTCCGCTACTTCCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 263
Qy 81 PheHisCysIleSerArgTyrLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 264 TTCACCTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGCAACAGAGAG 323

QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 324 TGGGAATTCCTCAAAAGTATGGGCAC 347

RESULT 4

US-10-085-783A-35025
; Sequence 35025, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35025
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-35025

Alignment Scores:
Pred. No.: 2,896-74 Length: 453
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-35025 (1-453)

QY 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyValAlaGlyLysLys 20
DB 24 ATGGCGGAGGATGGATGGATACCCGCGGCGCACCAACAGCGGCGGCGGCAAG 83
QY 21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 84 CGCTTTGAAGTGAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGAT 143
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 144 AACTGTGCCATCTCGCAGGAACACACATTATGGATCTTTGCATAGAAATGTCAAGCTAACCCAG 203
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 204 GCGTCCGCTACTTCAGAAAGTGTACTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC 263
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 264 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAG 323
QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 324 TGGGAATTCCTCAAAAGTATGGGCAC 347

RESULT 5

US-10-242-535A-39933
; Sequence 39933, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A

; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39933
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-39933

Alignment Scores:
Pred. No.: 3,016-74 Length: 467
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-39933 (1-467)

QY 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyValAlaGlyLysLys 20
DB 20 ATGGCGGAGGATGGATGGATACCCGCGGCGCACCAACAGCGGCGGCGGCAAG 79
QY 21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 80 CGCTTTGAAGTGAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGAT 139
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 140 AACTGTGCCATCTCGCAGGAACACACATTATGGATCTTTGCATAGAAATGTCAAGCTAACCCAG 199
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 200 GCGTCCGCTACTTCAGAAAGTGTACTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC 259
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAG 319
QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 320 TGGGAATTCCTCAAAAGTATGGGCAC 343

RESULT 6

US-10-085-783A-39933
; Sequence 39933, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39933
; LENGTH: 467
; TYPE: DNA

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; ORGANISM: Human
US-10-085-783A-39933

Alignment Scores:
Pred. No.: 3,01e-74 Length: 467
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-39933 (1-467)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
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Db 20 ATGGCGGCGAGTGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAG 76

QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
   |||||
Db 80 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT 139

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
   |||||
Db 140 AACTGTGCCATCTGCAGAACCAACATTTATGGATCTTTGCATAGAAATGCTCAAGCTAACCCAG 199

QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
   |||||
Db 200 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 259

QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
   |||||
Db 260 TTCACATGCAATCTCTCGCTGGCTCAAAACACGACAGGTGTCTCCATTGGACACAGAGAG 319

QY 101 TrpGluPheGlnLysTyrGlyHis 108
   |||||
Db 320 TGGGAATTCCAAAGTATGGGCAC 343

RESULT 7
US-10-242-535A-57254
; Sequence 57254, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-57254

Alignment Scores:
Pred. No.: 3,05e-74 Length: 471
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-57254 (1-471)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
   |||||
Db 17 ATGGCGGCGAGTGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAG 76

QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
   |||||
Db 77 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT 136

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
   |||||
Db 137 AACTGTGCCATCTGCAGAACCAACATTTATGGATCTTTGCATAGAAATGCTCAAGCTAACCCAG 196

QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
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Db 137 AACTGTGCCATCTGCAGAACCAACATTTATGGATCTTTGCATAGAAATGCTCAAGCTAACCCAG 196

US-10-085-783A-57254
; Sequence 57254, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-57254

Alignment Scores:
Pred. No.: 3,05e-74 Length: 471
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-57254 (1-471)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
   |||||
Db 17 ATGGCGGCGAGTGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAG 76

QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
   |||||
Db 77 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGGTTGAT 136

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
   |||||
Db 137 AACTGTGCCATCTGCAGAACCAACATTTATGGATCTTTGCATAGAAATGCTCAAGCTAACCCAG 196

QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
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Db 137 AACTGTGCCATCTGCAGAACCAACATTTATGGATCTTTGCATAGAAATGCTCAAGCTAACCCAG 196
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Db      197 GCGTCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 255
Qy      81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db      257 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGAGTGCTGCCATTGGACACACAGAG 316
Qy      101 TrpGluPheGlnLysTyR GlyHis 108
Db      317 TGGGAATTCCAAAAGTATGGGCAC 340

RESULT 9
US-10-242-535A-56068
; Sequence 56068, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C. C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56068
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-56068

Alignment Scores:
Pred. No.: 3,06e-74 Length: 472
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-56068 (1-472)
Qy      1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db      20 ATGGCGGCAGCATGTGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCACAGAG 79
Qy      21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db      80 CGCTTTGAAGTCAAAAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 139
Qy      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db      140 AACTGTGCATCTCGAGGAACCAATTATGGATCTTTGCATAGATGTCTCAAGCTAACACG 199
Qy      61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db      200 GCGTCGCTACTTCAGAAAGTGTACTGTCCATGGGGAGTCTGTAAACCATGCTTTTCAC 259
Qy      81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100

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;; PRIOR APPLICATION NUMBER: US 60/305,340
;; PRIOR FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: US 60/275,017
;; PRIOR FILING DATE: 2001-03-12
;; PRIOR APPLICATION NUMBER: US 60/271,955
;; PRIOR FILING DATE: 2001-02-28
;; NUMBER OF SEQ ID NOS: 58994
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 46292
;; LENGTH: 523
;; TYPE: DNA
;; ORGANISM: Human
US-10-242-535A-46292

Alignment Scores:
Pred. No.: 3.52e-74 Length: 523
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-46292 (1-523)

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Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
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Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 139 AACTGTGCCATCTCTCAGAAAGTGAATGCAAGTGGATCTCTGGGCTGGGATATTGTGGTTGAT 138
Qy 61 AlaSerAlaThrSerGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 199 GCGTCCGCTACTTCAAGAACCACTATGATCTTTGCATAGATGTCAAGCTAACCAAG 198
Qy 61 AlaSerAlaThrSerGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 199 GCGTCCGCTACTTCAAGAACCACTATGATCTTTGCATAGATGTCAAGCTAACCAAG 198
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 259 TTCACATGCAATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAG 318
Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 319 TGGGAATTCAAAAGTATGGGCAC 342

RESULT 14

US-10-085-783A-46292
; Sequence 46292, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46292
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-46292

Alignment Scores:
Pred. No.: 3.52e-74 Length: 523
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-46292 (1-523)

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Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 79 CGCTTTGAAGTGAAGTGAATGCAAGTGGATCTCTGGGCTGGGATATTGTGGTTGAT 138
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 139 AACTGTGCCATCTCTCAGAAAGTGAATGCAAGTGGATCTCTGGGCTGGGATATTGTGGTTGAT 138
Qy 61 AlaSerAlaThrSerGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 199 GCGTCCGCTACTTCAAGAACCACTATGATCTTTGCATAGATGTCAAGCTAACCAAG 198
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 259 TTCACATGCAATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAG 318
Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 319 TGGGAATTCAAAAGTATGGGCAC 342

RESULT 15

US-09-918-995-17191
; Sequence 17191, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17191
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(476)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-17191

Alignment Scores:
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Score: 611.00 Matches: 107
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.2% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-918-995-17191 (1-476)

Qy 2 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArg 21
Db 75 GCGGCGAGTGGATGTGGATACCCGAGCGGCACCAACAGCGCGGGCAAGAAGCGC 134

GenCore version 5.1.7
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Run on: March 15, 2006, 08:51:24 ; Search time 2486 Seconds
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2469.466 Million cell updates/sec

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Perfect score: 108

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Word size: 12

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Post-processing: Listing first 45 summaries

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-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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3: gb.env:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	108	100.0	433	6	CQ698451 Sequence
3	108	100.0	453	6	CQ690099 Sequence

	4	108	100.0	467	6	CQ695007	Sequence
5	108	100.0	471	6	CQ712328	Sequence	
6	108	100.0	472	6	CQ711142	Sequence	
7	108	100.0	482	6	BD027641	Sequence	
8	108	100.0	482	6	AX888031	Sequence	
9	108	100.0	504	6	BD271522	VonHippel	
10	108	100.0	504	6	AR640605	Sequence	
11	108	100.0	504	9	AF140599	Mus muscu	
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13	108	100.0	508	6	BD271520	VonHippel	
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17	108	100.0	531	9	BC001473	Mus muscu	
18	108	100.0	535	8	BC001466	Homo sapi	
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21	108	100.0	1612	9	BC056992	Mus muscu	
22	108	100.0	1616	9	BC027396	Mus muscu	
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25	103	95.4	4476	6	CQ493737	Sequence	
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ALIGNMENTS

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LOCUS
DEFINITION Homo sapiens RING finger protein (ROCI) mRNA, complete cds.
ACCESSION AF142059
VERSION AF142059.1 GI:4809215
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 327)
Ohta,T., Michel,J.J., Schottelius,A.J. and Xiong,Y.
TITLE ROCI, a homolog of APC1, represents a family of cullin partners
with an associated ubiquitin ligase activity
JOURNAL Mol. Cell 3 (4), 535-541 (1999)
PUBMED 10230407
REFERENCE 2 (bases 1 to 327)
Ohta,T., Michel,J.J. and Xiong,Y.
TITLE Direct Submission
JOURNAL Submitted (10-APR-1999) Lineberger Comprehensive Cancer Center,
University of North Carolina at Chapel Hill, Mason Farm Rd. and
Manning Dr., Chapel Hill, NC 27599-7295, USA
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 LOCUS CO695007 467 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 39933 from Patent WO02070737.
 ACCESSION CO695007
 VERSION CO695007.1 GI:42240530
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 REFERENCE 1
 AUTHORS Liew C.C., Marshall, W.E. and Zhang, H.
 TITLE Compositions and methods relating to osteoarthritis
 JOURNAL Patent: WO 02070737-A 39933 12-SEP-2002;
 Chondrogene Inc. (CA)
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 Db 80 CGCTTTGAAGTGAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 139
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 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 Db 200 GCGTCCGCTACTTTCAGAGAGTGACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 259
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Db 260 TTCACCTGCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 319
 Qy 101 TrpGluPheGlnLysTrpGlyHis 108
 Db 320 TGGGAATTCCTCAAAAGTATGGGCAC 343
 RESULT 5
 LOCUS CO712328 471 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 57254 from Patent WO02070737.
 ACCESSION CO712328
 VERSION CO712328.1 GI:42273185
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 REFERENCE 1
 AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
 TITLE Compositions and methods relating to osteoarthritis
 JOURNAL Patent: WO 02070737-A 57254 12-SEP-2002;
 Chondrogene Inc. (CA)
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 Qy 101 TrpGluPheGlnLysTrpGlyHis 108
 Db 317 TGGGAATTCCTCAAAAGTATGGGCAC 340
 RESULT 6
 LOCUS CO711142 472 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 56068 from Patent WO02070737.
 ACCESSION CO711142
 VERSION CO711142.1 GI:42271999
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 56068 12-SEP-2002;
Chondrogene Inc. (CA)

FEATURES
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/mol_type="unassigned DNA"
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ORIGIN

Alignment Scores: 2.41e-112 Length: 472
Pred. No.: 108.00 Matches: 108
Score: 108.00 Conservative: 0
Percent Similarity: 100.0%
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x CQ711142 (1-472)

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QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 80 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 139
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 140 AACTGTGCCATCTGCAGAACCAACATATGATGATCTTTGCATAGAACTCAAGTACAC 199
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 200 GCGTCCGCTACTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAACTGCTTTTTCAC 259
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 260 TTCACATGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATGGCAACAGAGAG 319
QY 101 TrpGluPheGlnLysTrpGlyHis 108
DB 320 TGGGAATTCAAAAGTATGGGCAC 343

RESULT 7
BD027641
LOCUS BD027641 482 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD027641
VERSION BD027641.1 GI:22569383
KEYWORDS JP 2001269182-A/3887.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 482)
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 3887 02-OCT-2001;
GENSET

COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/3887
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES JORDAN

PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40

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FH Key Location/Qualifiers
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Location/Qualifiers
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Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

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QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
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QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 89 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 148
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 149 AACTGTGCCATCTGCAGAACCAACATATGATGATCTTTGCATAGAACTCAAGTACAC 208
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 209 GCGTCCGCTACTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAACTGCTTTTTCAC 268
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 269 TTCACATGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATGGCAACAGAGAG 328
QY 101 TrpGluPheGlnLysTrpGlyHis 108
DB 329 TGGGAATTCAAAAGTATGGGCAC 352

RESULT 8
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LOCUS AX888031 482 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3894 from Patent EP1033401.
ACCESSION AX888031
VERSION AX888031.1 GI:40046785
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 3894 06-SEP-2000;
GENSET (FR)

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CDS


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Query Match: 100.0% Indels: 0
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Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
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Qy 41 AsnCyAlaAlaLeuCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 138 AACTGTGCCATCTGCAGGAACCAATATGATCTTTGATCGAATGTCAGGCCAACCCAG 197

Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 198 GCCTCAGCTACTTCCGAAGAGTGACGGTTGCATGGGAGTCTGCCAACCAATGCTTTTCAT 257

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 258 TTCCACTGCATCTCTCGATGGCTCAAAACGAGGAGGTGTCTCGTTGGACACAGAGAG 317

Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 318 TGGGAGTTCCAGAAGTATGGGCAT 341

RESULT 11
AF140599
LOCUS Mus musculus 504 bp mRNA linear ROD 11-MAY-1999
DEFINITION Mus musculus ring-box protein 1 (Rbx1) mRNA, complete cds.
ACCESSION AF140599
VERSION AF140599.1 GI:4769005
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Kamura,T., Koepf,D.M., Conrad,M.N., Skowrya,D., Moreland,R.J.,
Ilipoulos,O., Lane,W.S., Kaelin,W.G. Jr., Elledge,S.J.,
Conaway,R.C., Harper,J.W. and Conaway,J.W.
TITLE Rbx1, a component of the VHL tumor suppressor complex and SCF
ubiquitin ligase
JOURNAL Science 284 (5414), 657-661 (1999)
PUBMED 10213691
REFERENCE 2 (bases 1 to 504)
AUTHORS Kamura,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma
Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA
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18..344
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ubiquitin ligase"
/codon_start=1
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/protein_id="AAD29716.1"
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CRNIMDLCEQANQASATSECTVAGVGNHAFHFCISRWLKTQVCELDNREWE
FKYGH"

ORIGIN
Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20

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Alignment Scores: 2.55e-112 Length: 504
Pred. No.: 108.00 Matches: 108
Score: 100.0% Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 100.0%
DB: 9 Gaps: 0

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US-09-541-462B-2 (1-108) x AF140599 (1-504)

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Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 78 CGCTTTGAAGTTAAAGTGAATGCAATGCGGCTTGGGCTTGGGACATTTGGTTGAT 137

Qy 41 AsnCyAlaAlaLeuCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 138 AACTGTGCCATCTGCAGGAACCAATATGATCTTTGATCGAATGTCAGGCCAACCCAG 197

Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 198 GCCTCAGCTACTTCCGAAGAGTGACGGTTGCATGGGAGTCTGCCAACCAATGCTTTTCAT 257

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 258 TTCCACTGCATCTCTCGATGGCTCAAAACGAGGAGGTGTCTCGTTGGACACAGAGAG 317

Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 318 TGGGAGTTCCAGAAGTATGGGCAT 341

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RESULT 12

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LOCUS Mus musculus 507 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 15833 from Patent WO02068579.
ACCESSION CQ729899
VERSION CQ729899.1 GI:42302243
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 15833 06-SEP-2002;
PE Corporation (NY) (US)
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ORIGIN

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Score: 100.0% Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 100.0%
DB: 6 Gaps: 0

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US-09-541-462B-2 (1-108) x CQ729899 (1-507)

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Db      7  ATGGCGGCGAGCGATGATGATGATACCCCGAGCGGCACCAACAGCGCGCGGCGCAAGAG 66
Qy      21 ArgPheGluValLysLysTTPAsnAlaValAlaLeuTTPAlaTTPAspIleValValAsp 40
Db      67 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 126
Qy      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db      127 AACTGTGCGCATCTCGAGAAACACATTAATGATCTTTGCATAGAAATGTCAGACTAACAG 186
Qy      61 AlaSerAlaThrSerGluGluCysThrValAlaTTPGlyValCysAsnHisAlaPheHis 80
Db      187 GCGTCCGCTACTTCAGAGAGTGTACTGTCGATGGGAGTGTGTACCATGCTTTTCAC 246
Qy      81 PheHisCysIleSerArgTTPLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db      247 TTCCACTGTCATCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGACACAGAGAG 306
Qy      101 TrpGluPheGlnLysTyrGlyHis 108
Db      307 TGGGAATTCACAAAGATATGGGCAC 330

RESULT 13
LOCUS   BD271520 508 bp DNA linear PAT 17-JUL-2003
DEFINITION VonHippel-Lindau tumor suppressor complex and novel component of SCF ubiquitin ligase.
ACCESSION BD271520
VERSION   BD271520.1 GI:33081288
KEYWORDS JP 2002541775-A/1.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 508)
AUTHORS   Conaway,J.W., Conaway,R.C. and Kamura,T.
TITLE     VonHippel-Lindau tumor suppressor complex and novel component of SCF ubiquitin ligase
JOURNAL   OKLAHOMA MEDICAL RESEARCH FOUNDATION
COMMENT   OS Homo sapiens (human)
          PN JP 2002541775-A/1
          PD 10-DEC-2002
          PR 25-FEB-2000 JP 2000601023
          PR 26-FEB-1999 US 60/121787
          PI JOAN W CONAWAY, RONALD C CONAWAY, TAKUMI KAMURA PC
          C12N15/09,A61K38/00,A61K38/53,A61K45/00,A61P35/00,C07K14/47, PC
          C12N1/15,
          C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12P21/02,G01N33/15,G01N33/PC
          50,
          PC G01N33/68
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Pred. No.: 2,57e-112 Length: 508
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x BD271520 (1-508)
Qy      1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyValaGlyLysLys 20
Db      7  ATGGCGGCGAGCGATGATGATGATACCCCGAGCGGCACCAACAGCGCGCGGCGCAAGAG 66
Qy      21 ArgPheGluValLysLysTTPAsnAlaValAlaLeuTTPAlaTTPAspIleValValAsp 40
Db      67 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 126
Qy      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db      127 AACTGTGCGCATCTCGAGAAACACATTAATGATCTTTGCATAGAAATGTCAGACTAACAG 186
Qy      61 AlaSerAlaThrSerGluGluCysThrValAlaTTPGlyValCysAsnHisAlaPheHis 80
Db      187 GCGTCCGCTACTTCAGAGAGTGTACTGTCGATGGGAGTGTGTACCATGCTTTTCAC 246
Qy      81 PheHisCysIleSerArgTTPLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db      247 TTCCACTGTCATCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGACACAGAGAG 306
Qy      101 TrpGluPheGlnLysTyrGlyHis 108
Db      307 TGGGAATTCACAAAGATATGGGCAC 330

RESULT 14
LOCUS   AR640603 508 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 3 from patent US 6858709.
ACCESSION AR640603
VERSION   AR640603.1 GI:62775412
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 508)
AUTHORS   Conaway,J.W., Conaway,R.C. and Kamura,T.
TITLE     Component of von Hippel-Lindau tumor suppressor complex and SCF ubiquitin ligase
JOURNAL   Patent: US 6858709-A 3 22-FEB-2005;
          Oklahoma Medical Research Foundation; Oklahoma City, OK
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Alignment Scores:
Pred. No.: 2,57e-112 Length: 508
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

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Db      67 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 126
Qy      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db      127 AACTGTGCGCATCTCGAGAAACACATTAATGATCTTTGCATAGAAATGTCAGACTAACAG 186
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Db 187 GCGTCGCTACTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 246
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 Db 247 TTCACATGCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCCATGGACACAGAG 306
 Qy 101 TrpGluPheGlnLysTyrGlyHis 108
 Db 307 TGGGAATTCAAAAGTATGGGCAC 330
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 LOCUS Homo sapiens ring-box protein 1 (RBX1) mRNA, complete cds.
 DEFINITION AF140598
 ACCESSION AF140598
 VERSION AF140598.1 GI:4769003
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 508)
 AUTHORS Kamura,T., Koepf,D.M., Conrad,M.N., Skowry,D., Moreland,R.J.,
 Iliopoulos,O., Lane,W.S., Kaelin,W.G. Jr., Elledge,S.J.,
 Conway,R.C., Harper,J.W. and Conaway,J.W.
 RBX1, a component of the VHL tumor suppressor complex and SCF
 ubiquitin ligase
 TITLE Science 284 (5414), 657-661 (1999)
 JOURNAL 10213691
 PUBMED 2 (bases 1 to 508)
 REFERENCE Kamura,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.
 AUTHORS Direct Submission
 TITLE Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma
 JOURNAL Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA
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 Pred. No.: 2,57e-112 Length: 508
 Score: 108.00 Matches: 108
 Percent Similarity: 100.0% Conservative: 0
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 Db 67 CGCTTTGAGTGAAGTGAAGTGAATGCATAGCCCTCTGGGCTGGGATATTGTGTTGAT 126

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 Db 127 AACTGTGCCATCTGCAGGAACACACATTATGGATCTTTGCATAGAATGTCAAGCTAACCCAG 186
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 Db 187 GCGTCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 Db 247 TTCACATGCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCCATGGACACAGAG 306
 Qy 101 TrpGluPheGlnLysTyrGlyHis 108
 Db 307 TGGGAATTCAAAAGTATGGGCAC 330
 RESULT 16
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 LOCUS Homo sapiens 523 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 46292 from Patent WO02070737.
 ACCESSION CO701366
 VERSION CO701366.1 GI:42262133
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1
 AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
 TITLE Compositions and methods relating to osteoarthritis
 JOURNAL Patent: WO 02070737-A 46292 12-SEP-2002;
 Chondrogene Inc. (CA)
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 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 6 Gaps: 0
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 Db 79 CGCTTTGAGTGAAGTGAAGTGAATGCATAGCCCTCTGGGCTGGGATATTGTGTTGAT 138
 Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
 Db 139 AACTGTGCCATCTGCAGGAACACCATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAG 198
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 Db 199 GCGTCGCTACTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 258
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 Db 259 TTCACATGCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCCATGGACACAGAG 318
 Qy 101 TrpGluPheGlnLysTyrGlyHis 108
 Db 319 TGGGAATTCAAAAGTATGGGCAC 342

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RESULT 17
BC051473
LOCUS
DEFINITION
Mus musculus ring-box 1, mRNA (cdna clone MGC:62905 IMAGE:1430400),
complete cds.
ACCESSION
BC051473
VERSION
BC051473.1 GI:30186056
KEYWORDS
MGC.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 531)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
JOURNAL
PUBMED
2 (bases 1 to 531)
DIRECTOR MGC Project.
AUTHORS
Direct Submission
TITLE
Submitted (28-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
Contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAP Plate: 113 Row: e Column: 22
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 40254545.
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FQKYGH"
ORIGIN
Alignment Scores: 2.69e-112 Length: 531
Pred. No.: 108.00 Matches: 108
Score: 100.0% Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 100.0% Gaps: 0
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QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 73 CGCTTTGAAGTTAAAGAGTGAATGCAATGAGTGGCCCTCTGGGCGCTGGACATTTGGTTGAT 132
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGluAlaAsnGln 60
Db 133 AACTGTGCCATCTCGAGAACCAACATATGGAATCTTTGTATCGAATGTGCAGCCCAACAG 192
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 193 CGCTCAGCTACTTCCGAGAGAGTGACGGTTGCATGGGAGGAGTCTGCAACCATGCTTTTCAT 252
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 253 TTCCACTGCATCTCTCGATGGCTCAAAACGAGCGAGGTGTGTCGCTGGACACAGAGAG 312
QY 101 TrpGluPheGlnLysTrpGlyHis 108
Db 313 TGGGAGTTCAGAGAGTATGGGCAT 336
RESULT 18
BC001466
LOCUS
DEFINITION
Homo sapiens ring-box 1, mRNA (cdna clone MGC:1481 IMAGE:3138751),
complete cds.
ACCESSION
BC001466
VERSION
BC001466.2 GI:34783098
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 535)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
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19. .345
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Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
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Db 79 CGCTTTGAAGTCGAAAGATGGATGACCTCTGGGCTCGGATATTGTGGTTGAT 138
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Db 139 AACTGTGCATCTCGCTGGCTCAAAACACACAGAGGTGTGTCCATTGGACACAGAGAG 198
Oy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 199 GCGTCCGCTACTTCAGAGAGGTGTACTGTGCGATGGGAGGTCTGTAAACATGCTTTTTCAC 258
Oy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 259 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGGTGTGTCCATTGGACACAGAGAG 318
Oy 101 TrpGluPheGlnLysTyrGlyHis 108
Db 319 TGGGAATTCCTCAAAAGTAGTGGGCAC 342

RESULT 20
BC017370 554 bp mRNA linear PRI 21-OCT-2003
LOCUS Homo sapiens ring-box 1, mRNA (cdna clone IMAGE:4065797), partial
DEFINITION cds.
ACCESSION BC017370
VERSION BC017370.1 GI:16924201
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 554)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

```

TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REMARK
 COMMENT

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whitton, M., Touchman, J.W., Green, E.D.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 554)
 Strausberg, R.
 Direct Submission
 Submitted (13-NOV-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amandasytemsbio.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha
 Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 19 Row: C Column: 17
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 [Posttranslational modification, protein turnover,
 chaperones / Cell division and chromosome partitioning]"
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FEATURES
 source

gene

CDS

misc_feature

ORIGIN

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 Percent Similarity: 100.0% Conservatives: 0
 Best Local Similarity: 100.0% Mismatches: 0
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 DB: 8 Gaps: 0

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 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 Db 203 GCCTCCGCTACTCTCAGAAGAGTGTACTGTGCGATGGGAGTCTGTACCAATGCTTTTCAC 262
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 Db 263 TTCACATGCATCTCTCGCTGCTCMAACACGACGAGTGTGTCATTTGGACACACAGAG 322
 Qy 101 TrpGluPheGlnLysTrpGlyHis 108
 Db 323 TGGGAATTCAAAAGTAGTGGGCAC 346

RESULT 21
 BC056992 1612 bp mRNA linear ROD 25-JUL-2005
 LOCUS Mus musculus ring-box 1, mRNA (cdna clone MGC:66938 IMAGE:6818827),
 DEFINITION complete cds.

ACCESSION BC056992.1 GI:34784939
 VERSION BC056992
 KEYWORDS MGC.
 SOURCE Mus musculus
 ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
 Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 JOURNAL 12477932
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1612)

AUTHORS
 CONSRM
 TITLE
 JOURNAL
 REMARK
 COMMENT

NIH MGC Project
 Direct Submission
 Submitted (25-AUG-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Genome Sequencing Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcgsc.bc.ca
 Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
 Pang, Diana Mah, Jing Wang, Kiech Fichtel, Eric Chuah, Allen
 Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
 Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
 Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis DelRio, Ruth
 Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
 Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR
 Santos, Duane Smal, Jeff Stott, Miranda Tsai, George Yang,
 Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
 Series: IRAK Plate: 126 Row: e Column: 20
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gene

CDS

ORIGIN

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Qy 101 TrpGluPheGlnLysTrpGlyHis 108
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RESULT 22

BC027396 1616 bp mRNA linear ROD 08-MAR-2005

LOCUS Mus musculus ring-box 1, mRNA (cdna clone MGC:35907 IMAGE:4952242), complete cds.

DEFINITION BC027396

ACCESSION BC027396.1 GI:20072075

VERSION MGC.

KEYWORDS Mus musculus (house mouse)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1616)

Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SP, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SJ, Wang J, Heish P, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Kettman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butlerfield YS, Krzywinski MI, Skaleka U, Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.

Mammalian Gene Collection Program Team

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1616)

Director MGC Project.

Direct Submission

Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

cDNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

CONSRMT

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

JOURNAL

REMARK

COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAP plate: 60 Row: 1 Column: 8

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 40254545.

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CDS

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ORIGIN

Alignment Scores:

Pred. No.: 7.27e-112 Length: 1616

Score: 108.00 Matches: 108

Percent Similarity: 100.0% Conservatve: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 9 Gaps: 0

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Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
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Db 127 AACTGTGCCATCTGCAGGAACACCATATATGATCTTTGTATCGAATGTTCAGGCCAACAG 186
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Qy 61 AlaSerAlaThrSerGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
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Db 247 TTCACATGCATCTCTCGATGGCTCAAAACGAGGCGAGGTGTGTCCTGGACACACAGAG 306
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Qy 101 TrpGluPheGlnLysTrpGlyHis 108
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Db 307 TGGGAGTTCACGAAGTATGGGCAT 330
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Job time : 2491 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2006, 08:44:10 ; Search time 166 Seconds
(without alignments)
1156.486 Million cell updates/sec

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Perfect score: 108
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Word size: 12

Total number of hits satisfying chosen parameters: 15

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=issued patents NA -QFMT=fastap -SUFFIX=oligo.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	108	100.0	507	3	US-09-949-016-4940
4	108	100.0	508	3	US-09-914-324A-3
5	84	77.8	3208	3	US-09-780-016-27
6	84	77.8	3208	3	US-10-214-811-27
7	84	77.8	3208	3	US-10-766-074-27
8	74	68.5	411	3	US-09-640-211A-1731
9	55	50.9	402	3	US-09-513-999C-10371

10 55 50.9 463 3 US-09-621-976-15180 Sequence 15180, A
11 40 37.0 301 3 US-09-313-294A-492 Sequence 492, App
12 29 26.9 25274 3 US-09-949-016-16682 Sequence 16682, A
13 12 11.1 480 3 US-09-914-324A-4 Sequence 4, Appl
14 12 11.1 490 3 US-09-270-767-26812 Sequence 26812, A
15 12 11.1 1101 3 US-09-270-767-11265 Sequence 11265, A

ALIGNMENTS

RESULT 1
US-09-513-999C-3894
; Sequence 3894, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3894
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29..352
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 404
; OTHER INFORMATION: m=a or c
US-09-513-999C-3894

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Pred. No.: 1.37e-109 Length: 482
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-513-999C-3894 (1-482)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 29 ATGCGCGCAGCGATGGATGATACCCGAGCGGCACCAACAGCGCGGGGCAAGAG 88
Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 89 CGCTTTGAAGTGAAGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGAT 148
Qy 41 AsnCyAlaAlaCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 149 AACTGTGCCATCTGCAGGAACCAACATTATGATGATCTTTGCATAGAAATGCAAGCTAACCCAG 208
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 209 GCGTCGCGTACTTTCAGAGAGAGTACTGTGCGATGGGAGTCTGTACCAATGCTTTTTCAC 268
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 269 TTCACATGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTTGGACACAGAGAG 328

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QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 329 TGGGAATTCACAAAGTATGGGCAC 352

RESULT 2
US-09-914-324A-5
; Sequence 5, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(344)
; OTHER INFORMATION: Rbx1
US-09-914-324A-5

Alignment Scores:
Pred. No.: 1,42e-109 Length: 504
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-914-324A-5 (1-504)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 18 ATGGCGGGCGGATGGATGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAAG 77
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLeuValValAsp 40
DB 78 CGCTTTGAAGTTAAAGTGAATGCAGTGGCCCTCTGGGCGTGGGACATTGGTTGAT 137
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 138 AACTGTGCCATCTCAGCAAGCAACCATATGGATCTTTGTATCGAATGTCAGGCCAACAG 197
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 198 CGGTCACTACTTCCAGAGAGTGACGGTTGCATGGGAGTCTGCACCATGCTTTTCAT 257
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 258 TTCCACTGCATCTCTCGATGCTCAAAACAGGAGGAGTGTCTCGTTGGACACAGAGAG 317
QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 318 TGGGAGTTCAGAAAGTATGGGCAT 341

RESULT 3
US-09-949-016-4940
; Sequence 4940, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4940
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4940

Alignment Scores:
Pred. No.: 1,43e-109 Length: 507
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-949-016-4940 (1-507)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 7 ATGGCGGGCGGATGGATGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAAG 66
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLeuValValAsp 40
DB 67 CGCTTTGAAGTGAAGTGAATGCAGTGGCCCTCTGGGCGTGGGATATGGTTGAT 126
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 127 AACTGTGCCATCTCAGCAAGCAACCATATGGATCTTTGGCATAGAAATGTCAGGTAACAG 186
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 187 GCCTCGCTACTTCAAGAGAGTGTACTGTCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 247 TTCCACTGCATCTCTCGTGGCTCAAAACAGCAGCAGGTGTGTCCATTGGACACAGAGAG 306
QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 307 TGGGAATTCACAAAGTATGGGCAC 330

RESULT 4
US-09-914-324A-3
; Sequence 3, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25

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QY 45 CysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaSerAlaThr 64
Db 2830 TGCAGGAACACATTATGGATCTTTGCATAGATGTCAGCTAACAGCGGTCCGCTACT 2889

QY 65 SerGluGluCysThrValAlaLLeuTrpGlyValCysAsnHisAlaPheHisCysIle 84
Db 2890 TCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCACTGCATC 2949

QY 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGln 104
Db 2950 TCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGTGGGAATCCAA 3009

QY 105 LysTyrGlyHis 108
Db 3010 AAGTATGGGCAC 3021

RESULT 7
US-10-766-074-27
; Sequence 27, Application US/10766074
; Patent No. 6881563
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6881563el Human Proteases and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10766,074
; PRIOR FILING DATE: 2004-01-28
; PRIOR FILING DATE: US/10/214,811
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-074-27

Alignment Scores:
Pred. No.: 1.71e-82 Length: 3208
Score: 84.00 Matches: 84
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 77.8% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-766-074-27 (1-3208)

QY 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIle 44
Db 2770 AAAAATGGAATGAGTAGAGCTTTGGCGCTGGATATTGGTTGATACCTGTGCCATC 2829

QY 45 CysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaSerAlaThr 64
Db 2830 TGCAGGAACACATTATGGATCTTTGCATAGATGTCAGCTAACAGCGGTCCGCTACT 2889

QY 65 SerGluGluCysThrValAlaLLeuTrpGlyValCysAsnHisAlaPheHisCysIle 84
Db 2890 TCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCACTGCATC 2949

QY 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGln 104
Db 2950 TCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGTGGGAATCCAA 3009
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QY 105 LysTyrGlyHis 108
Db 3010 AAGTATGGGCAC 3021

RESULT 8
US-09-640-211A-1731
; Sequence 1731, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: Modification of Gene Transcription
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1731
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Pinus radiata
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(411)
; OTHER INFORMATION: n = A, T, C or G
US-09-640-211A-1731

Alignment Scores:
Pred. No.: 2.49e-72 Length: 411
Score: 74.00 Matches: 74
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 68.5% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-640-211A-1731 (1-411)

QY 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIle 44
Db 176 AAGAAGTGAATGCTGTAGCCCTTGGCGTGGATATTGGTTGATATAATTGTGCAATT 235

QY 45 CysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaSerAlaThr 64
Db 236 TGCAGAAACACATCATGGACCTCTGTATTGAGTGTGAGCAATCAAGCAAGTGCACAA 295

QY 65 SerGluGluCysThrValAlaLLeuTrpGlyValCysAsnHisAlaPheHisCysIle 84
Db 296 AGTGAAGAATGTACTGTTGCATGGGGTGTTCATATCAGCCCTTTCATTTCCATTGCATA 355

QY 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsn 98
Db 356 AGTCGGTGGCTCAAGACACGACAGTCTGCCCATTTAGATAAT 397

RESULT 9
US-09-513-999C-10371
; Sequence 10371, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
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; SEQ ID NO 16682
; LENGTH: 25274
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16682

Alignment Scores:
Pred. No.: 2,66e-21 Length: 25274
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 26.9% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-949-016-16682 (1-25274)

Qy 77 HisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeu 96
Db 18411 CATGCTTTTTCACITTCCTCACTGCACTCTCGCTGGCTCAAAACACGACGAGGTGTGTCATG 18470

Qy 97 AspAsnArgGluTrpGluPheGlnLys 105
Db 18471 GACACAGACAGTGGGAATTCCTCAAAAG 18497

RESULT 13
US-09-914-324A-4
; Sequence 4, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklamoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(369)
; OTHER INFORMATION: Rbx1
US-09-914-324A-4

Alignment Scores:
Pred. No.: 0.00033 Length: 480
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-914-324A-4 (1-480)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 157 GTTGACAACTGTGTATTGTCAGGAACCATATAATG 192

RESULT 14
US-09-767-26812/c
; Sequence 26812, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11265
; LENGTH: 1101
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11265

Alignment Scores:
Pred. No.: 0.000704 Length: 1101
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-270-767-11265 (1-1101)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 867 GTTGACAACTGTGCCATCTGCCGTAAACCATCATG 832

Search completed: March 11, 2006, 09:40:59
Job time : 171 secs
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; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26812
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26812

Alignment Scores:
Pred. No.: 0.000337 Length: 490
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-270-767-26812 (1-490)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 256 GTTGACAACTGTGCCATCTGCCGTAAACCATCATG 221

RESULT 15
US-09-270-767-11265/c
; Sequence 11265, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11265
; LENGTH: 1101
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11265

Alignment Scores:
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Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-270-767-11265 (1-1101)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 867 GTTGACAACTGTGCCATCTGCCGTAAACCATCATG 832
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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
1367.677 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 108

Sequence: 1 MAAAMDVTPGTSNGAGK.....KTRQVCPDLNREWFQYGH 108

Scoring table:

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 12

Total number of hits satisfying chosen parameters: 119

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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-DB=Published_Applications_NA_Main -QFMT=fastcap -SUFFIX=oligo.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=12
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs03h
-USER=US09541462@CGN_1_1026@runat_10032006_080844_22623 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	108	100.0	433	7	US-10-242-535A-43377
2	108	100.0	433	7	US-10-085-783A-43377
3	108	100.0	453	7	US-10-242-535A-35025
4	108	100.0	453	7	US-10-085-783A-35025
5	108	100.0	467	7	US-10-242-535A-39933
6	108	100.0	467	7	US-10-085-783A-39933
7	108	100.0	471	7	US-10-242-535A-57254

8	108	100.0	471	7	US-10-085-783A-57254
9	108	100.0	472	7	US-10-242-535A-56068
10	108	100.0	472	7	US-10-085-783A-56068
11	108	100.0	504	8	US-10-913-937-5
12	108	100.0	508	8	US-10-913-937-3
13	108	100.0	523	8	US-10-242-535A-46292
14	108	100.0	523	7	US-10-085-783A-46292
15	107	99.1	476	3	US-09-918-995-17191
16	106	98.1	4543	5	US-10-198-846-11311
17	103	95.4	4476	8	US-10-357-930-25604
18	98	90.7	3484	8	US-10-723-860-1383
19	98	90.7	3484	9	US-10-756-149-1357
20	98	90.7	5111	5	US-10-205-823-382
21	98	90.7	5111	10	US-11-051-454-382
22	98	90.7	5371	8	US-10-723-860-5852
23	95	88.0	430	7	US-10-242-535A-54751
24	95	88.0	430	7	US-10-085-783A-54751
25	90	83.3	468	7	US-10-242-535A-47656
26	90	83.3	468	7	US-10-085-783A-47656
27	90	83.3	5347	6	US-10-240-965-99
28	87	80.6	380	3	US-09-960-352-4677
29	84	77.8	3208	3	US-09-780-016-27
30	84	77.8	3208	5	US-10-214-811-27
31	84	77.8	3208	7	US-10-766-074-27
32	84	77.8	3208	10	US-11-036-185-27
33	83	76.9	692	10	US-11-097-143-31031
34	74	68.5	411	8	US-10-856-499-1731
35	74	68.5	527	9	US-10-487-901-4266
36	74	68.5	531	9	US-10-487-901-4271
37	74	68.5	617	9	US-10-487-901-4265
38	74	68.5	619	7	US-10-425-114-25647
39	74	68.5	673	9	US-10-487-901-4262
40	74	68.5	731	9	US-10-487-901-4264
41	74	68.5	840	7	US-10-767-701-12172
42	70	64.8	390	3	US-09-770-791-20
43	70	64.8	553	7	US-10-021-323-10545
44	70	64.8	608	8	US-10-767-795-687
45	70	64.8	831	8	US-10-767-795-2752

ALIGNMENTS

RESULT 1

US-10-242-535A-43377
; Sequence 43377, Application US/10242535A
; Publication No. US20040013663A1

; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43377
; LENGTH: 433
; TYPE: DNA

; ORGANISM: Human
US-10-242-535A-43377

Alignment Scores:

Pred. No.: 9.41e-111 Length: 433
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-43377 (1-433)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 DB 20 ATGGCGGACGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
 QY 21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 DB 80 CGCTTTGAAGTGAAAGTGGATGCAAGTACCTCTGGGCGCTGGGATATTTGGTTGAT 139
 QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
 DB 140 AACTGTGCCATCTGCAGGACCAACATATATGATGATGATGATGATGATGATGATGAT 199
 QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 DB 200 CGGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC 259
 QY 81 PheHisCysIleSerArgTyrLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 DB 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGCAACAGAGAG 319
 QY 101 TrpGluPheGlnLysTyrGlyHis 108
 DB 320 TGGGAATTCAAAAGATATGGGCAC 343

RESULT 2

US-10-085-783A-43377
 ; Sequence 43377, Application US/10085783A
 ; Publication No. US20040037841A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2002
 ; CURRENT APPLICATION NUMBER: US/10/085,783A
 ; CURRENT FILING DATE: 2002-02-28
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 43377
 ; LENGTH: 433
 ; TYPE: DNA
 ; ORGANISM: Human

US-10-085-783A-43377

Alignment Scores:
 Pred. No.: 9,41e-111 Length: 433
 Score: 108.00 Matches: 108
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-43377 (1-433)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 DB 20 ATGGCGGACGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
 QY 21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 DB 80 CGCTTTGAAGTGAAAGTGGATGCAAGTACCTCTGGGCGCTGGGATATTTGGTTGAT 139

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
 DB 140 AACTGTGCCATCTGCAGGACCAACATATATGATGATGATGATGATGATGATGATGAT 199
 QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 DB 200 CGGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC 259
 QY 81 PheHisCysIleSerArgTyrLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 DB 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGCAACAGAGAG 319
 QY 101 TrpGluPheGlnLysTyrGlyHis 108
 DB 320 TGGGAATTCAAAAGATATGGGCAC 343

RESULT 3

US-10-242-535A-35025
 ; Sequence 35025, Application US/10242535A
 ; Publication No. US20040013663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2005
 ; CURRENT APPLICATION NUMBER: US/10/242,535A
 ; CURRENT FILING DATE: 2002-09-12
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 35025
 ; LENGTH: 453
 ; TYPE: DNA
 ; ORGANISM: Human

US-10-242-535A-35025

Alignment Scores:
 Pred. No.: 9,79e-111 Length: 453
 Score: 108.00 Matches: 108
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-35025 (1-453)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 DB 24 ATGGCGGACGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 83
 QY 21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 DB 84 CGCTTTGAAGTGAAAGTGGATGCAAGTACCTCTGGGCGCTGGGATATTTGGTTGAT 143
 QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
 DB 144 AACTGTGCCATCTGCAGGACCAACATATATGATGATGATGATGATGATGATGATGAT 203
 QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 DB 204 CGGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC 263
 QY 81 PheHisCysIleSerArgTyrLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 DB 264 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGCAACAGAGAG 323


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; ORGANISM: Human
US-10-085-783A-39933

Alignment Scores:
Pred. No.:      Length:      467
Score:          Matches:     108
Percent Similarity: 100.0%   Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:    Indels:     0
DB:             Gaps:       0

US-09-541-462B-2 (1-108) x US-10-085-783A-39933 (1-467)

QY      1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db      20 ATGGCGGCAGCATGGATGTGGATACCCGAGCGGCCAACACAGCGCGCGCAAGAAG 79
QY      21 ArgPheGluValLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db      80 CGCTTTGAAGTGAATAAGTGGAATCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 139
QY      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysGlnAlaAsnGln 60
Db      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysGlnAlaAsnGln 60

QY      61 AlaSerAlaThrSerGluCuCysThrValAlaLeuTrpGlyValCysAsnHisAlaPheHis 80
Db      140 AACTGTGCCATCTGCAGGAACACATTATGGATCTTCGATAGATGTCAAGCTTAACCAG 199
QY      61 AlaSerAlaThrSerGluCuCysThrValAlaLeuTrpGlyValCysAsnHisAlaPheHis 80
Db      200 GCCTCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTCAC 259
QY      81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db      260 TTCACACTGCATCTCGCTGGCTCAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 319
QY      101 TrpGluPheGlnLysTyrglyHis 108
Db      320 TGGGAATTCAAAAGTATGGGCAC 343

RESULT 7
US-10-242-535A-57254
; Sequence 57254, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-57254

Alignment Scores:
Pred. No.:      Length:      471
Score:          Matches:     108
Percent Similarity: 100.0%   Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:    Indels:     0
DB:             Gaps:       0

US-09-541-462B-2 (1-108) x US-10-242-535A-57254 (1-471)

QY      1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db      17 ATGGCGGCAGCATGGATGTGGATACCCGAGCGGCCAACACAGCGCGCGCAAGAAG 76
QY      21 ArgPheGluValLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db      77 CGCTTTGAAGTGAATAAGTGGAATCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 136
QY      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysGlnAlaAsnGln 60
Db      137 AACGTGCCATCTGCAGGAACACATTATGGATCTTCGATAGATGTCAAGCTTAACCAG 196
QY      61 AlaSerAlaThrSerGluCuCysThrValAlaLeuTrpGlyValCysAsnHisAlaPheHis 80
Db      61 AlaSerAlaThrSerGluCuCysThrValAlaLeuTrpGlyValCysAsnHisAlaPheHis 80

US-09-541-462B-2 (1-108) x US-10-085-783A-57254 (1-471)

QY      1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db      17 ATGGCGGCAGCATGGATGTGGATACCCGAGCGGCCAACACAGCGCGCGCAAGAAG 76
QY      21 ArgPheGluValLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db      77 CGCTTTGAAGTGAATAAGTGGAATCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 136
QY      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysGlnAlaAsnGln 60
Db      137 AACGTGCCATCTGCAGGAACACATTATGGATCTTCGATAGATGTCAAGCTTAACCAG 196
QY      61 AlaSerAlaThrSerGluCuCysThrValAlaLeuTrpGlyValCysAsnHisAlaPheHis 80

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; ORGANISM: Human
 US-10-085-783A-39933
 Alignment Scores:
 Pred. No.: 1,01e-110 Length: 467
 Score: 108.00 Matches: 108
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0
 US-09-541-462B-2 (1-108) x US-10-085-783A-39933 (1-467)
 QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 DB 20 ATGGCGGCGAGCGATGGATGCGATACCCGAGCGGCAACACAGCGCGCGGCAAGAAG 79
 QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 DB 80 CGCTTTGAAGTGAAGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 139
 QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuValLeuGluCysGlnAlaAsnGln 60
 DB 140 AACTGTGCCATCTGCAGGAACACACATTATGGATCTTGGGCTGGGATATTGTGGTTGAT 199
 QY 61 AlaSerAlaThrSerGluCysThrValAlaLeuTrpGlyValCysAsnHisAlaPheHis 80
 DB 200 GCGTCGCTACTTCAGAGAGTGTACTGTCGATGGGAGTCTGTAACCATGCTTTTTCAC 259
 QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 DB 260 TTCCACTGCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGCAACACAGAGAG 319
 QY 101 TrpGluPheGlnLysTyrGlyHis 108
 DB 320 TGGGAATTCAAAAGTATGGGCAC 343
 RESULT 7
 US-10-242-535A-57254
 ; Sequence 57254, Application US/10242535A
 ; Publication No. US20040013663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2005
 ; CURRENT FILING DATE: 2002-09-12
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 10/085,783
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 57254
 ; LENGTH: 471
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-242-535A-57254
 Alignment Scores:
 Pred. No.: 1,01e-110 Length: 471
 Score: 108.00 Matches: 108
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0
 US-09-541-462B-2 (1-108) x US-10-242-535A-57254 (1-471)
 QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 DB 17 ATGGCGGCGAGCGATGGATGCGATACCCGAGCGGCAACACAGCGCGCGGCAAGAAG 76
 QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 DB 77 CGCTTTGAAGTGAAGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 136
 QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuValLeuGluCysGlnAlaAsnGln 60
 DB 137 AACTGTGCCATCTGCAGGAACACACATTATGGATCTTGGCATTAGATGTCAAGCTAACCCAG 196
 QY 61 AlaSerAlaThrSerGluCysThrValAlaLeuTrpGlyValCysAsnHisAlaPheHis 80

Db 197 CGCTCCGCTACTTCAGAAAGAGTGTACTTCGCATGGGAGTGTGAACCATGCTTTTCAC 256
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 257 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACACAGAG 316
Qy 101 TrpGluPheGlnLysTyrglyHis 108
Db 317 TGGGAATTCCAAAGATATGGGCAC 340

RESULT 9

US-10-242-535A-56068
; Sequence 56068, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56068
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a, c, g, or t

US-10-242-535A-56068

Alignment Scores:
Pred. No.: 1.02e-110 Length: 472
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-56068 (1-472)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20
Db 20 ATGGCGGCGAGTGATGTGGATACCCCGAGCGGCACCAACAGCGCGGCAAGAG 79
Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 80 CGCTTTGAAGTGAAGAGTGAATGCAGTACCCCTCTGGGCTGGGATATTGTGTTGAT 139
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGlyCysGlnAlaAsnGln 60
Db 140 AACGTGTGCATCTCGCAGGAACCACTATGATCTTTGCATAGAAATGTCAAGCTAACCCAG 199
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 200 GCGTCCGCTACTTCAGAAAGAGTGTACTGTGCGCATGGGAGTGTGAACCATGCTTTTCAC 259
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100

Db 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACACAGAG 319
Qy 101 TrpGluPheGlnLysTyrglyHis 108
Db 320 TGGGAATTCCAAAGATATGGGCAC 343

RESULT 10

US-10-085-783A-56068
; Sequence 56068, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56068
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a, c, g, or t

US-10-085-783A-56068

Alignment Scores:
Pred. No.: 1.02e-110 Length: 472
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-56068 (1-472)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20
Db 20 ATGGCGGCGAGTGATGTGGATACCCCGAGCGGCACCAACAGCGCGGCAAGAG 79
Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 80 CGCTTTGAAGTGAAGAGTGAATGCAGTACCCCTCTGGGCTGGGATATTGTGTTGAT 139
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGlyCysGlnAlaAsnGln 60
Db 140 AACGTGTGCATCTCGCAGGAACCACTATGATCTTTGCATAGAAATGTCAAGCTAACCCAG 199
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 200 GCGTCCGCTACTTCAGAAAGAGTGTACTGTGCGCATGGGAGTGTGAACCATGCTTTTCAC 259
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACACAGAG 319
Qy 101 TrpGluPheGlnLysTyrglyHis 108
Db 320 TGGGAATTCCAAAGATATGGGCAC 343

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RESULT 11
US-10-913-937-5
; Sequence 5, Application US/10913937
; Publication No. US20050019813A1
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/10/913,937
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US/09/914,324
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/10/913,937
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US/09/914,324
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(344)
; OTHER INFORMATION: Rbx1
US-10-913-937-5
Alignment Scores:
Pred. No.: 1.08e-110 Length: 504
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-913-937-5 (1-504)
Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 18 ATGGCGCGCGGATGGATGGATACCCCGCGGACCAACAGCGCGCGGCAAGAG 77
Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLeuValVal 40
Db 78 CGCTTTGAAGTAAAGTGAATGCAGTGGCCCTCTGGGCGCTGGGACATTTGGTTGAT 137
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 138 AACTGTGCCATCTCCAGAACCAACATTTATGGATCTTTGTATCGAATGTCAGGCCAACAG 197
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 198 GCGTCAGTACTTCCGAAGAGTGTACGTTGCATGGGAGTCTGCAACCATGCTTTTCAT 257
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 258 TTCCACTGCATCTCTCGATGCTCAAAACGAGGAGGTGTCTCCGTTGGACAAACAGAGAG 317
Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 318 TGGGAGTTCCAAAGTATGGGCAT 341

RESULT 12
US-10-913-937-3
; Sequence 3, Application US/10913937
; Publication No. US20050019813A1
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.

```

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; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/10/913,937
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US/09/914,324
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(333)
; OTHER INFORMATION: Rbx1
US-10-913-937-3
Alignment Scores:
Pred. No.: 1.08e-110 Length: 508
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-913-937-3 (1-508)
Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 7 ATGGCGCGCGGATGGATGGATACCCCGCGGACCAACAGCGCGCGGCAAGAG 66
Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLeuValVal 40
Db 67 CGCTTTGAAGTAAAGTGAATGCAGTGGCCCTCTGGGCGCTGGGATATTGGTTGAT 126
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 127 AACTGTGCCATCTCCAGAACCAACATTTATGGATCTTTGCATAGAGATGTCAGCTAAC 186
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 187 GCGTCCCTACTTCCAGAACAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTT 246
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 247 TTCCACTGCATCTCTCGCTGCTCAAAACAGCAGGTGTGTCCATTGGACAAACAGAG 306
Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 307 TGGGAATTCAAAAGTATGGGCAC 330

RESULT 13
US-10-242-535A-46292
; Sequence 46292, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28

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; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 46292
 ; LENGTH: 523
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-242-535A-46292

Alignment Scores:
 Pred. No.: 1.11e-110 Length: 523
 Score: 108.00 Matches: 108
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-46292 (1-523)

Qy 1 MetalaalaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 Db 19 ATGGCGGCGAGTGGATGTGGATACCCCGAGCGGCACCAACAGCGCGGCAAGAAG 78
 Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 Db 79 CGCTTTGAAGTGAAGAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 138
 Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGln 60
 Db 139 AACTGTGCCATCTCAGAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 138
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 Db 199 GCGTCCGCTACTTCCAGAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 138
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 Db 259 TTCACCTGCATCTCTCGCTGCTCAAAACACGACGAGTGTGTCCATTGGACACAGAGAG 318
 Qy 101 TrpGluPheGlnLysTrpGlyHis 108
 Db 319 TGGGAATTCAAAAGTATGGGCAC 342

RESULT 14

US-10-085-783A-46292
 ; Sequence 46292, Application US/10085783A
 ; Publication No. US20040037841A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liaw, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2002
 ; CURRENT APPLICATION NUMBER: US/10/085,783A
 ; CURRENT FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 46292
 ; LENGTH: 523
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-085-783A-46292

Alignment Scores:
 Pred. No.: 1.11e-110 Length: 523
 Score: 108.00 Matches: 108
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-46292 (1-523)

Qy 1 MetalaalaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 Db 19 ATGGCGGCGAGTGGATGTGGATACCCCGAGCGGCACCAACAGCGCGGCAAGAAG 78
 Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 Db 79 CGCTTTGAAGTGAAGAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 138
 Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGln 60
 Db 139 AACTGTGCCATCTCAGAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 138
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
 Db 199 GCGTCCGCTACTTCCAGAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 138
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 Db 259 TTCACCTGCATCTCTCGCTGCTCAAAACACGACGAGTGTGTCCATTGGACACAGAGAG 318
 Qy 101 TrpGluPheGlnLysTrpGlyHis 108
 Db 319 TGGGAATTCAAAAGTATGGGCAC 342

RESULT 15

US-09-918-995-17191
 ; Sequence 17191, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 17191
 ; LENGTH: 476
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(476)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-17191

Alignment Scores:

Pred. No.: 1.34e-109 Length: 476
 Score: 107.00 Matches: 107
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 99.1% Indels: 0
 DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-918-995-17191 (1-476)

Qy 2 AlaalaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArg 21
 Db 75 GCGGCGGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGGCAAGAAGCGC 134

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QY 22 PheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsn 41
Db 135 TTTGAAGTGAATAAGTGAATGCAGTAGCCCTCTGGGCCTGGGATATTTGGTTGATAAC 194
QY 42 CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla 61
Db 195 TGTGCCATCTGCAGGAACCACTATTGGATCTTTGCATAGAAATGTCAGCTAACCCAGGCG 254
QY 62 SerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPhe 81
Db 255 TCCGCTACTTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAACCATGCTTTTCACCTC 314
QY 82 HisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrp 101
Db 315 CACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGATGG 374
QY 102 GluPheGlnLysTyrGlyHis 108
Db 375 GAATTCCAAAGTATGGGCAC 395

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Search completed: March 11, 2006, 10:04:09
Job time : 655 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2006, 08:30:45 ; Search time 494 Seconds
(without alignments)
1457.058 Million cell updates/sec

Title: US-09-541-462B-2
Perfect score: 108
Sequence: 1 MAAAMDVTSGTNGAGKK.....KTRQVCPDNRNWFQYKH 108

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Word size: 12

Total number of hits satisfying chosen parameters: 95

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=N_Geneseq -QFMT=fastap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=12 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abas03h
-USR=US09541462 @CGN 1 1 727 @runat_10032006_080830_22345 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -BSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*
- 14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	108	100.0	327	3 AAA96882	Aaa96882 Nucleotid
2	108	100.0	482	3 AAC03896	Aaac03896 Human sec
3	108	100.0	504	3 AAA74980	Aaa74980 DNA encod
4	108	100.0	506	12 ADQ87496	Adq87496 Human tum

5	108	100.0	506	12	ADQ87156	Adq87156 Human tum
6	108	100.0	506	13	ADQ84881	Adq84881 Human tum
7	108	100.0	508	3	AAA74978	Aaa74978 DNA encod
8	108	100.0	508	13	ACN40951	Acn40951 Tumour-as
9	107	99.1	476	9	ACH29979	Ach29979 Human tes
c 10	106	98.1	3726	13	ADS09913	Ads09913 Human the
c 11	106	98.1	4543	11	ACN90161	Acn90161 Breast ca
c 12	105	97.2	503	12	ADQ92179	Adq92179 Human aut
13	105	97.2	539	5	AAH97860	Aah97860 Murine 7-
14	105	97.2	586	5	AAH97862	Aah97862 Murine 7-
c 15	103	95.4	4476	5	ABV25615	Abv25615 Human pro
c 16	98	90.7	311	14	ACL57420	Act57420 Human col
c 17	98	90.7	3484	12	ADF42703	Adf42703 Human tes
c 18	98	90.7	3484	12	ADQ18564	Adq18564 Human sof
c 19	98	90.7	3484	13	ADQ80865	Adq80865 Human SPA
c 20	98	90.7	5111	10	ADB75558	Adb75558 Prostate
c 21	98	90.7	5371	12	ADQ23032	Adq23032 Human sof
c 22	90	83.3	485	3	AAA43288	Aaa43288 Xenopus s
c 23	90	83.3	5347	6	AAS94844	Aas94844 Human DNA
c 24	87	80.6	380	8	ABX39512	Abx39512 Bovine ES
25	84	77.8	3208	4	AAD12859	Aad12859 Human nov
26	83	76.9	692	4	ABL22527	Abi22527 Drosophil
27	74	68.5	411	3	AAC57009	Aac57009 Pinus rad
28	74	68.5	527	10	ADK56883	Adk56883 Plant DNA
29	74	68.5	531	10	ADK56888	Adk56888 Plant DNA
30	74	68.5	617	10	ADK56882	Adk56882 Plant DNA
31	74	68.5	619	13	ADX50907	Adx50907 Plant ful
32	74	68.5	673	10	ADK56879	Adk56879 Plant DNA
33	74	68.5	721	14	AEB66106	Aeb66106 Rice geno
34	74	68.5	731	10	ADK56881	Adk56881 Plant DNA
c 35	72	66.7	502	14	ADY78665	Ady78665 Human CDN
36	70	64.8	390	6	ABQ85150	Abq85150 Arabidops
c 37	70	64.8	553	13	ACN55764	Actn55764 Cotton an
38	70	64.8	608	13	ADR59906	Adr59906 Cotton cd
39	70	64.8	635	3	AAC39854	Aac39854 Arabidops
40	70	64.8	831	13	ADR61971	Adr61971 Cotton cd
41	69	63.9	509	5	AAS68845	Aas68845 DNA encod
42	67	62.0	586	10	ADK56887	Adk56887 Plant DNA
43	67	62.0	691	10	ADK56880	Adk56880 Plant DNA
44	66	61.1	2841	4	ABL22526	Abi22526 Drosophil
45	58	53.7	342	12	ADG99381	Adg99381 Kidney di

ALIGNMENTS

RESULT 1

AAA96882
ID AAA96882 standard; DNA; 327 BP.

XX
AC AAA96882;

DT 19-FEB-2001 (first entry)

XX Nucleotide sequence of human ring finger protein ROC1.

DE ROC1; ROC2; cullin; ring finger protein; APC11; APC complex; SCF pathway;
KW cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation;
KW tumour; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..327

FT /*tag= a

FT /product= "ROC1"

XX WO200058472-A2.

XX PD 05-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US008592.

XX PR 31-MAR-1999; 99US-0127261P.

Db 329 TGGGAATTCCTCAAAAGTATGGGCAC 352
RESULT 3
AAA74980
ID AAA74980 standard; DNA; 504 BP.
AC AAA74980;
XX
DT 02-JAN-2001 (first entry)
DE DNA encoding a murine cullin-interacting RING-H2 finger protein (Rbx1).
XX Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
KW tumour suppressor; carcinoma; Ring box associated carcinoma;
KW von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
KW cerebellar hemangioblastoma; hemangioma; retinal angioma;
KW pheochromocytoma; ss.
XX
OS Mus sp.
XX
FN WO200050445-A1.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000WO-US004838.
XX
PR 26-FEB-1999; 99US-0121787P.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
PI Conaway JA, Conaway RC, Kamura T;
XX
DR WPI; 2000-572067/53.
XX
PT Cullin interacting RING-H2 finger protein, a component of von Hippel-Lindau tumor suppressor complex and Skp1-Cdc53p-F-box protein (SCF) ubiquitin ligase, useful for diagnosing and treating Ring box protein associated carcinomas.
XX
PS Disclosure; Page 35; 37pp; English.
XX
CC The present sequence encodes a murine cullin-interacting RING-H2 finger protein (Ring box protein), designated Rbx1. The human Rbx1 polypeptide is a tumour suppressor. Human Rbx1 is useful for diagnosing a predisposition of a patient to certain carcinomas. It is also useful for treating Ring box protein associated carcinomas or augmenting metabolically deficient system in animals. Human Rbx1 is also useful for evaluating the effectiveness of a therapeutic treatment for Ring box associated carcinomas. Human Rbx1 can be used to screen for agents which augment or inhibit the activity of other cullin-containing ubiquitin ligase and of the VHL (von Hippel-Lindau) complex controlling the conjugation of ubiquitin or ubiquitin-like proteins to various sets of target proteins. Carcinomas which may be treated include renal carcinomas, cerebellar hemangioblastomas and hemangiomas, retinal angioma and pheochromocytomas
XX
SQ Sequence 504 BP; 117 A; 107 C; 137 G; 143 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,72e-106 Length: 504
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-09-541-462b-2 (1-108) x AAA74980 (1-504)
Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLeuLys 20
Db 18 ATGGCGCGCGCGATGGTGTGGATACCCCGACGGCCACCAACAGCGCGCGGCAAGAG 77

Qy 21 ArgPheGluValLysLysTTPAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 78 CGCTTTGAAGTTAAAAAGTGAATGCAATGCGAGTGGCCCTCTGGGCTGGACATTGTGTTGAT 137
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 138 AACTGTGCCATCTCGAGAACCACTATATGATCTTTGTATCGAATGTTCAGGCCAACAG 197
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 198 GCGTCAGCTACTTCCGAAGAGTGTACGGTTCATGGGAGTCTGCAACCATGCTTTTCAT 257
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 258 TTCCATGCTCATCTCTCGATGCTCAAAACGAGGAGGTGTGTCGTTGGACACAGAGAG 317
Qy 101 TrpGluPheGlnLysTyrGlyHis 108
Db 318 TGGGAGTTCCAGAAAGTATGGGCAT 341
RESULT 4
ADQ87496
ID ADQ87496 standard; CDNA; 506 BP.
XX
AC ADQ87496;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4374.
XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
OS Homo sapiens.
XX
FN WO2004060270-A2.
XX
PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
XX
PR 18-OCT-2002; 2002US-0418988P.
XX
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
PI Wu TD, Zhou Y;
XX
DR WPI; 2004-534300/51.
XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
PS Claim 1; SEQ ID NO 4374; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a

CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAR binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAR sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAR cDNA sequence from the present invention.
XX
SQ Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,73e-106 Length: 506
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 12 Gaps: 0

US-09-541-462B-2 (1-108) x ADQ87496 (1-506)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 6 ATGGCGGCGAGTGGATGGATGGATACCCCGAGCGGCACCAACGCGCGCGGCAAG 65
Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 66 CGCTTTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 125
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 126 AACTGTGCGCATCTGCAGGAACCAATATGATCTTTGCATAGAAATGCTCAAGCTAAC 185
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 186 GCGTCCGCTACTTCAGAAAGAGTGTACTGTGCGATGGGAGTGTGTAAACCATGCTTTT 245
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 246 TTCACATGTCATCTCGCTGGCTCAAAACAGCAGAGTGTGTCCATTGGACACAGAG 305
Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 306 TGGGAATTCAAAAGTATGGGCAC 329

RESULT 5
ADQ87156
ID ADQ87156 standard; cDNA; 506 BP.
XX
AC ADQ87156;

XX 07-OCT-2004 (first entry)
XX Human tumour-associated antigenic target (TAT) cDNA sequence #4032.
DE human; tumour-associated antigenic target; TAR; cytostatic; gene therapy;
XX human; tumour-associated antigenic target; TAR; cytostatic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.
OS Homo sapiens.
XX

PN WO2004060270-A2.
XX
PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
XX
PR 18-OCT-2002; 2002US-0418988P.
XX
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
PI Wu TD, Zhou Y;
XX
XX WPI; 2004-534300/51.
DR
XX
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
XX Claim 1; SEQ ID NO 4032; 5504pp; English.
XX

CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAR binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAR sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAR cDNA sequence from the present invention.
XX
SQ Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,73e-106 Length: 506
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 12 Gaps: 0

US-09-541-462B-2 (1-108) x ADQ87156 (1-506)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20

Db ATGGCGGAGCATGGATGGATATCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 65
Qy 21 ArgPheGluValLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db CGCTTTGAAGTGAAAGAGTGAATGACAGTACCTCTGGGCTGGGATATTGGTTGAT 125
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 126 AACTGTGCATCTGCAGGAACACACATTATGGATCTTTGCATAGAAATGTCAAGCTAACCCAG 185
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 186 GCGTCCGCTACTTCAGAGAGTGTAATGTCATGGGAGTCTGTAAACCATGCTTTTCAC 245
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 246 TTCCACTCACTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAGAG 305
Qy 101 TrpGluPheGlnLysTyrGlyHis 108
Db 306 TGGGAATTCCTCAAAAGTATGGGCAC 329

RESULT 6

ADQ84881

ID ADQ84881 standard; cDNA; 506 BP.

XX AC ADQ84881;
XX DT 07-OCT-2004 (first entry)XX DE Human tumour-associated antigenic target (TAT) cDNA sequence #1695.
XX KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
XX KW cancer; cell proliferative disorder; gene; ss.

XX OS Homo sapiens.

XX PN WO2004060270-A2.

XX PD 22-JUL-2004.

XX PF 15-OCT-2003; 2003WO-US029126.

XX PR 18-OCT-2002; 2002US-0418988P.

XX PA (GETH) GENENTECH INC.
XX PA (WUTD/) WU T D.

XX PI (ZHOU/) ZHOU Y.

XX PI Wu TD, Zhou Y;

XX DR WPI; 2004-534300/51.

XX PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
XX PT preventing or treating cell proliferative disorders such as cancer.
XX PS Claim 1; SEQ ID NO 1695; 5504pp; English.

XX The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process

CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.

XX SQ Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,73e-106 Length: 506
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-09-541-462B-2 (1-108) x ADQ84881 (1-506)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 6 ATGGCGGAGCATGGATGGATATCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 65
Qy 21 ArgPheGluValLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 66 CGCTTTGAAGTGAAAGAGTGAATGACAGTACCTCTGGGCTGGGATATTGGTTGAT 125
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 126 AACTGTGCATCTGCAGGAACACACATTATGGATCTTTGCATAGAAATGTCAAGCTAACCCAG 185
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 186 GCGTCCGCTACTTCAGAGAGTGTAATGTCATGGGAGTCTGTAAACCATGCTTTTCAC 245
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 246 TTCCACTCACTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAGAG 305
Qy 101 TrpGluPheGlnLysTyrGlyHis 108
Db 306 TGGGAATTCCTCAAAAGTATGGGCAC 329

RESULT 7

AAA74978

ID AAA74978 standard; DNA; 508 BP.

XX AC AAA74978;
XX DT 02-JAN-2001 (first entry)

XX DE DNA encoding a human cullin-interacting RING-H2 finger protein (Rbx1).

XX KW Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
XX tumour suppressor; carcinoma; Ring box associated carcinoma;

KW von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
 KW cerebellar hemangioblastoma; hemangioma; retinal angioma;
 KW pheochromocytomas; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..333
 FT /*tag= a
 FT /product= "cullin-interacting RING-H2 finger protein
 FT (Rbx1)"
 XX
 PN WO200050445-A1.
 XX
 XX 31-AUG-2000.
 XX
 XX 25-FEB-2000; 2000WO-US004838.
 XX
 XX 26-FEB-1999; 99US-0121787P.
 XX
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 XX
 XX Conway JA, Conway RC, Kamura T;
 XX
 XX WPI; 2000-572067/53.
 DR P-PSDB; AAB08813.
 XX
 XX Cullin interacting RING-H2 finger protein, a component of von Hippel-
 PT Lindau tumor suppressor complex and Skp1-Cdc53p-P-box protein (SCP)
 PT ubiquitin ligase, useful for diagnosing and treating Ring box protein
 PT associated carcinomas.
 XX
 XX Claim 3; Page 35; 37pp; English.
 XX
 XX The present sequence encodes a human cullin-interacting RING-H2 finger
 CC protein (Ring box protein), designated Rbx1. The polypeptide is a tumour
 CC suppressor. Rbx1 is useful for diagnosing a predisposition of a patient
 CC to certain carcinomas. It is also useful for treating Ring box protein
 CC associated carcinomas or augmenting metabolically deficient system in
 CC animals. Rbx1 is also useful for evaluating the effectiveness of a
 CC therapeutic treatment for Ring box associated carcinomas. Rbx1 can be
 CC used to screen for agents which augment or inhibit the activity of other
 CC cullin-containing ubiquitin ligase and of the VHL (von Hippel-Lindau)
 CC complex controlling the conjugation of ubiquitin or ubiquitin-like
 CC proteins to various sets of target proteins. Carcinomas which may be
 CC treated include renal carcinomas, cerebellar hemangioblastomas and
 CC hemangiomas, retinal angioma and pheochromocytomas
 XX
 XX Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 2,74e-106 Length: 508
 Score: 108.00 Matches: 108
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0
 US-09-541-462B-2 (1-108) x AAA74978 (1-508)
 QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 DB 7 ATGGCGGAGGATGGATGGATACCCGCGGACCAACAGCGCGGCGGCAAGAAG 66
 QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 DB 67 CGCTTTGAAGTGAAAGTGAATGACAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 126
 QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
 DB 127 AACTGTGCATCTGCAGGACCAACATATTGATCTTTGCATAGATGTCAGCTAACCCAG 186
 QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80

DB 187 GCGTCGCTACTTCAGAGAGTGACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
 QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 DB 247 TTCCTACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACACAGAGAG 306
 QY 101 TrpGluPheGlnLysTyrGlyHis 108
 DB 307 TGGGAATTCCAAAGATATGGGCAC 330
 RESULT 8
 ACN40951
 ID ACN40951 standard; cDNA; 508 BP.
 XX
 AC ACN40951;
 XX
 XX 18-NOV-2004 (first entry)
 XX
 XX Tumour-associated antigenic target (TAT) cDNA DNA326980, SEQ ID NO:6072.
 XX
 KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO2004030615-A2.
 XX
 XX 15-APR-2004.
 XX
 XX 29-SEP-2003; 2003WO-US028547.
 XX
 XX 02-OCT-2002; 2002US-0414971P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Wu TD, Zhang Z, Zhou Y;
 XX
 XX WPI; 2004-347921/32.
 DR P-PSDB; ABM82365.
 XX
 XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 XX Claim 1; SEQ ID NO 6072; 7273pp; English.
 XX
 XX The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT nucleic acid of the invention

XX Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;
SQ Alignment Scores:
Pred. No.: 2.74e-106 Length: 508
Score: 108.00 Matches: 108
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0
US-09-541-462B-2 (1-108) x ACN40951 (1-508)
Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 7 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGAAGAAG 66
Qy 21 ArgPheGluValLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 67 CGCTTTGAAGTGAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 126
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 127 AACTGTGCCATCTGCAGAAACCAACATATGATCTTTCATAGATGTCAAGCTAACAG 186
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 187 GCGTCCGCTACTTCAGAAGAGTGTACTGTCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 247 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTCTCCATTGGACACAGAG 306
Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 307 TGGGAATTCAAAAGATATGGGCAC 330
RESULT 9
ACH29979
ID ACH29979 standard; cDNA; 476 BP.
XX ACH29979;
XX 13-OCT-2003 (first entry)
XX Human testis cDNA #365.
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
XX Homo sapiens.
XX US2003073623-A1.
XX 17-APR-2003.
XX 30-JUL-2001; 2001US-00918995.
XX 30-JUL-2001; 2001US-00918995.
XX (DRMA/) DRMANAC R T.
XX (LABA/) LABAT I.
XX (STAC/) STACHE-CRAIN B.
XX (DICK/) DICKSON M C.
XX (JONE/) JONES L W.
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX WPI; 2003-615964/58.
XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating

PT antisense DNA or RNA.
XX Claim 1; SEQ ID NO 17191; 44pp; English.
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH2789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antibodies specific for it. The present polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX SQ Sequence 476 BP; 119 A; 111 C; 124 G; 118 T; 0 U; 4 Other;
Alignment Scores:
Pred. No.: 3.05e-105 Length: 476
Score: 107.00 Matches: 107
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 9 Gaps: 0
US-09-541-462B-2 (1-108) x ACH29979 (1-476)
Qy 2 AlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArg 21
Db 75 GCGGACGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGAAGCGC 134
Qy 22 PheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsn 41
Db 135 TTTGAAGTGAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATAAC 194
Qy 42 CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla 61
Db 195 TGTGCCATCTGCAGGAACCAACATATGATCTTTCATAGATGTCAAGCTAACCGCG 254
Qy 62 SerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPhe 81
Db 255 TCCGCTACTTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTC 314
Qy 82 HisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrp 101
Db 315 CACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGTGG 374
Qy 102 GluPheGlnLysTrpGlyHis 108
Db 375 GAATTCAAAAGATATGGGCAC 395
RESULT 10
ADS09913/c
ID ADS09913 standard; DNA; 3726 BP.
XX ADS09913;
XX 16-DEC-2004 (first entry)
XX Human therapeutic DNA - SEQ ID 150.
XX antiinflammatory; neuroprotective; antianemic; cytostatic; vulnerary;
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
XX Homo sapiens.

XX WO2004080148-A2.
 PN
 XX
 XX 23-SEP-2004.
 PD
 XX
 XX 30-SEP-2003; 2003WO-US030720.
 PF
 XX
 XX 02-OCT-2002; 2002US-0416186P.
 PR
 XX
 XX (NUVE-) NUVELO INC.
 PA
 XX
 XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
 PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
 PI
 XX WPI; 2004-668857/65.
 DR P-PSDB; ADS10597.
 DR
 XX
 XX New polynucleotide, useful in preparing a composition for diagnosing or
 PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
 PT aplastic anemia or cancer for promoting wound healing.
 PT
 XX
 XX Claim 1; SEQ ID NO 150; 718pp; English.
 PS
 XX
 XX The invention relates to a novel isolated polynucleotide and the encoded
 CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
 CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
 CC be useful in preparing a composition for diagnosing or treating
 CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
 CC disorders, such as aplastic anaemia or cancer, as well as for promoting
 CC wound healing. The molecules may also be utilised during gene therapy
 CC procedures. The current sequence is that of a human therapeutic DNA of
 CC the invention. The current sequence is not shown explicitly within the
 CC specification but can be accessed from the WIPO web-site.
 CC
 XX
 SQ Sequence 3726 BP; 996 A; 955 C; 845 G; 930 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 2,43e-103 Length: 3726
 Score: 106.00 Matches: 106
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 98.1% Indels: 0
 DB: 13 Gaps: 0

US-09-541-462B-2 (1-108) x ADS09913 (1-3726)

Qy 3 AlaalaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPhe 22
 Db 492 GCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGGCGGCAAGCGCTTT 433
 Qy 23 GluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLysValValAspAsnCys 42
 Db 432 GAAGTGAAGAAGTGAATGCAGTAGCCCTCTGGCGCTGGGATATTGGTTGATAACTGT 373
 Qy 43 AlaileCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer 62
 Db 372 GCCATCTGCAGGAACCAACATTATGGATCTTTGCATAGAAATGCTCAAGCTAACCGCGTCC 313
 Qy 63 AlathrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 82
 Db 312 GCTACTTTCAGAAAGTAGTGTCTGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 253
 Qy 83 CysileSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGlu 102
 Db 252 TGCATCTCTCGTCTGCTCAAAACACGACAGAGTGTGTCCATTGGACACAGAGAGTGGAA 193
 Qy 103 PheGlnLysTyrGlyHis 108
 Db 192 TTCCAAAAGTATGGGCAC 175

RESULT 11
 ACN90161/c
 ID ACN90161 standard; DNA; 4543 BP.

XX ACN90161;
 AC
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Breast cancer related marker, seq id 11311.
 DE
 XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
 KW
 XX
 OS Homo sapiens.
 OS
 XX US2003099974-A1.
 PN
 XX
 XX 29-MAY-2003.
 PD
 XX
 XX 18-JUL-2002; 2002US-00198846.
 PF
 XX
 XX 18-JUL-2001; 2001US-0306220P.
 PR
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX
 XX Lillie J, Xu Y, Wang Y, Steinmann K;
 PI
 XX WPI; 2003-787014/74.
 DR
 XX
 XX Novel isolated polypeptide associated with breast cancer, useful for
 PT detecting presence of polypeptide in sample, as a marker for breast
 PT cancer.
 PT
 XX
 PS Disclosure; SEQ ID NO 11311; 36pp; English.
 XX
 CC The invention relates to an isolated polypeptide (I) associated with
 CC breast cancer which is encoded by a nucleic acid molecule comprising a
 CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
 CC the polypeptide of the invention. The activity of the polypeptide of the
 CC invention may be described as cytostatic. The antibody is useful for
 CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
 CC invention are useful in the detection of breast tumours. (I) is useful as
 CC a marker for breast cancer and in breast cancer therapy. Sequences given
 CC in records ACN78851-ACN92934 represent nucleic acid markers associated
 CC with breast cancer. Note: The sequence listing does not form part of the
 CC specification but may be obtained in electronic format from the USPTO web
 CC site at seqdata.uspto.gov/sequence.html?DocID=20030099974
 CC
 XX
 SQ Sequence 4543 BP; 1069 A; 1171 C; 1083 G; 1220 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 2,93e-103 Length: 4543
 Score: 106.00 Matches: 106
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 98.1% Indels: 0
 DB: 11 Gaps: 0

US-09-541-462B-2 (1-108) x ACN90161 (1-4543)

Qy 3 AlaalaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPhe 22
 Db 1085 GCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGGCGGCAAGCGCTTT 1026
 Qy 23 GluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLysValValAspAsnCys 42
 Db 1025 GAAGTGAAGAAGTGAATGCAGTAGCCCTCTGGCGCTGGGATATTGGTTGATAACTGT 966
 Qy 43 AlaileCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer 62
 Db 965 GCCATCTGCAGGAACCAACATTATGGATCTTTGCATAGAAATGCTCAAGCTAACCGCGTCC 906
 Qy 63 AlathrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 82
 Db 905 GCTACTTTCAGAAAGTAGTGTCTGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 846
 Qy 83 CysileSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGlu 102

Db 845 TCATCTTCGCTGGCTCAAAACACGACAGAGGTGTCCATTGGACACAGAGTGGGAA 786

Qy 103 PheGlnLysTyrGlyHis 108
Db 785 TTCCAAGAGTATGGGCAC 768

RESULT 12

ADQ92179
ID ADQ92179 standard; DNA; 503 BP.

AC ADQ92179;

XX 07-OCT-2004 (first entry)

XX Human autoantigen DNA fragment MPMGP800L05536.

XX ds; autoantigen; antibody; hybridoma; biosensor chip;
KW extracorporeal differential diagnosis; autoimmune disease;
KW ribosomal protein; tubulin;
KW dolichyl-diphospho-oligosaccharide-glycosyl transferase;
KW multiple sclerosis; rheumatoid arthritis; epitope mapping;
KW affinity chromatography; electrophoresis; autoantibody apheresis;
KW RNA interference, RNAi.

XX Homo sapiens.

XX WO2004058972-A1.

XX 15-JUL-2004.

XX 23-DEC-2002; 2002WO-EP014731.

XX 23-DEC-2002; 2002WO-EP014731.

XX (THIE/) THIESEN H.

XX (LORE/) LORENZ P.

XX Thiesen H, Lorenz P;

XX WPI; 2004-543459/52.

XX New human DNA autoantigens, useful as assay, diagnostic, and prognostic
PT reagents and for treating autoimmune disease, also related expression
PT products and antibodies with similar uses.

XX Claim 1; SEQ ID NO 160; 110pp; German.

XX This invention describes novel human DNA autoantigens which are used to
CC produce recombinant expression vectors; prokaryotic or eukaryotic cells;
CC poly- or mono-clonal antibodies (Ab) specific; hybridomas that express
CC monoclonal Ab; biosensor chips having an addressable sequence pattern as
CC probes; medical or diagnostic instruments that include the biosensor; for
CC extracorporeal differential diagnosis of autoimmune diseases and
CC proteins; tubulins; dolichyl-diphospho-oligosaccharide-glycosyl
CC transferases and proteins. The antibodies may be labelled conventionally
CC with radioisotopes, coloured or fluorescent groups, or a member of the
CC biotin/avidin pair, or colloidal gold. The autoantigens can be directed
CC against mitochondria, liver-kidney microsomes; histidyl-tRNA; nuclear
CC membrane; neurophilin/cytoplasm; insect cells; epidermal intracellular
CC or basal membrane antigens; Golgi or cell nuclei, or associated with
CC multiple sclerosis or rheumatoid arthritis. They are useful for epitope
CC mapping; in affinity chromatography or electrophoresis; for diagnosis,
CC prognosis, control of treatment or therapeutic response of autoimmune
CC diseases, particularly in vitro differential diagnosis of autoimmune
CC diseases; to produce biosensor chips or for autoantibody apheresis.
CC Autoantigen DNA can be used for therapeutic RNA interference against
CC autoantibodies. Biochips that carry the new materials are useful in
CC medical and diagnostic instruments. ADQ92020-ADQ92280 represent human
CC autoantigens.

XX Sequence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.47e-103 Length: 503
Score: 105.00 Matches: 105
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.2% Indels: 0
DB: 12 Gaps: 0

US-09-541-462B-2 (1-108) x ADQ92179 (1-503)

Qy 4 AlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGlu 23
Db 3 GCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGGCAAGCGCTTTGAA 62
Qy 24 VallyLysTyrAsnAlaValAlaLeuTrpAlaIleValValAspAsnCysAla 43
Db 63 GTGAAGAAGTGAATGCGATGAGCCCTCTGGCCCTGGGATATGTGTTGATAACTGTGCC 122
Qy 44 IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla 63
Db 123 ATCTGCAGGAACCACTATGATCTTTGCATAGATGCTCAAGCTAACCCAGCGTCCGCT 182
Qy 64 ThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHisAlaPheHisPheHisCys 83
Db 183 ACTTCAGAAGAGTGTACTGTGCGCATGGGGAGTCTGTAACCATGCTTTTCACTTCCACTGC 242
Qy 84 IleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPhe 103
Db 243 ATCTCTCGTGGCTCAAAACACGACAGGTGTGTCCTCATGGACAACAGAGTGGGAATTC 302
Qy 104 GlnLysTyrGlyHis 108
Db 303 CAAAAGTATGGGCAC 317

RESULT 13

AAH97860
ID AAH97860 standard; DNA; 539 BP.

XX AAH97860;

XX 10-OCT-2001 (first entry)

XX Murine 7-transmembrane G-protein coupled receptor coding sequence #104.

XX Murine; hematopoietic stem cell; signalling; vaccine; 7TM-GPCR;

XX 7-transmembrane G-protein coupled protein receptor; ds.

XX Mus sp.

XX WO200160999-A1.

XX 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US004700.

XX 14-FEB-2000; 2000US-0182377P.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX (UYPR-) UNIV PRINCETON.

XX Lemischka IR, Witte L, Pereira DS;

XX WPI; 2001-522596/57.

XX DNA Sequences encoding 7-transmembrane G-protein coupled protein
PT receptors characteristic of hematopoietic stem cells, useful for treating
PT leukemia.

XX Claim 1; Page 62; 176pp; English.

XX The present invention relates to murine coding sequences for 7-
CC transmembrane G-protein coupled protein receptors (7TM-GPCRs). The

XX 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX Schlegel R, Endege WO, Monahan JE;
 DR WPI; 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 PS Claim 1; Page 5119-5120; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 SQ Sequence 4476 BP; 1085 A; 1129 C; 1015 G; 1247 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4.75e-100 Length: 4476
 Score: 103.00 Matches: 103
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 95.4% Indels: 0
 DB: 5 Gaps: 0
 US-09-541-462B-2 (1-108) x ABV25615 (1-4476)
 Qy 3 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPhe 22
 Db 1014 GCAGCGATGGATGGATACCCCGAGCGGACCAACAGCGCGGGCAAGAGCGCTTT 955
 Qy 23 GluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAlaTrpAspIleValValAspAsnCys 42
 Db 954 GAAGTGAANAAGTGAATGCAGTAGCCCTCTGGGCGCTGGGATATTGTGTTGATACCTGT 895
 Qy 43 AlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer 62
 Db 894 GCCATCTGCAGAACCAACATTATGGATCTTTGCATAGAAATGTCAGCTAACCCAGCGCTCC 835
 Qy 63 AlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHis 82
 Db 834 GCTACTTCCAGAGAGTGTACTGTGCGATGGGAGTGTCTAAACCATGCTTTTCACTTCCAC 775
 Qy 83 CysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGlu 102
 Db 774 TGCATCTCTCGTGGCTCAAAACACGACAGGTGTGTCTTGGACACACAGAGATGGGAA 715
 Qy 103 PheGlnLys 105
 Db 714 TTCCAAAAA 706

Search completed: March 11, 2006, 09:53:11
 Job time : 501 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2006, 08:27:10 ; Search time 349 Seconds
(without alignments)
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Title: US-09-541-462B-2
Perfect score: 616
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-MAXLEN=200000000 -HOST=abs05h
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
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4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
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6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
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8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	527	85.6	660	9	US-11-096-568A-11809 Sequence 11809, A
2	516.5	83.8	432	9	US-11-096-568A-14405 Sequence 14405, A
3	515.5	83.7	693	9	US-11-096-568A-26820 Sequence 26820, A
4	499	81.0	348	9	US-11-096-568A-28569 Sequence 28569, A

5	385	62.5	366	7	US-10-932-182A-78459 Sequence 78459, A
6	385	62.5	366	7	US-10-932-182A-78459 Sequence 78459, A
7	381	61.9	366	7	US-10-932-182A-2279 Sequence 2279, Ap
8	381	61.9	366	7	US-10-932-182A-2279 Sequence 2279, Ap
9	292	47.4	342	8	US-10-821-234-554 Sequence 554, App
10	234	38.0	546	12	US-11-128-061-5740 Sequence 5740, Ap
11	234	38.0	546	12	US-11-128-049-5740 Sequence 5740, Ap
12	234	38.0	579	12	US-11-128-061-2098 Sequence 2098, Ap
13	234	38.0	579	12	US-11-128-049-2098 Sequence 2098, Ap
14	217	35.2	648	5	US-09-978-360A-4 Sequence 4, Appl
15	215	34.9	450	9	US-11-057-84A-14 Sequence 14, Appl
16	211	34.3	3404	12	US-11-045-468A-18 Sequence 18, Appl
c 17	196	31.8	153	7	US-10-932-182A-81177 Sequence 81177, A
c 18	196	31.8	153	7	US-10-932-182A-81177 Sequence 81177, A
c 19	195	31.7	420	8	US-10-821-234-360 Sequence 360, App
c 20	175	28.4	207	7	US-10-932-182A-6146 Sequence 6146, Ap
c 21	175	28.4	207	7	US-10-932-182A-6146 Sequence 6146, Ap
c 22	137.5	22.3	2135	9	US-11-072-512-459 Sequence 459, App
23	133	21.6	498	7	US-10-932-182A-75906 Sequence 75906, A
24	133	21.6	498	7	US-10-932-182A-75906 Sequence 75906, A
25	99	16.1	2027	9	US-11-096-568A-12921 Sequence 12921, A
26	95.5	15.5	752	9	US-11-096-568A-3548 Sequence 3548, Ap
27	95	15.4	922	9	US-11-096-568A-13533 Sequence 13533, A
28	93	15.1	808	9	US-11-096-568A-1239 Sequence 1239, Ap
29	91	14.8	76	8	US-10-310-914A-128 Sequence 128, App
30	91	14.8	76	8	US-10-310-914A-16478 Sequence 16478, A
31	91	14.8	683	9	US-11-096-568A-3705 Sequence 3705, Ap
32	91	14.8	1324	9	US-11-096-568A-3994 Sequence 3994, Ap
33	89.5	14.5	908	9	US-11-096-568A-5433 Sequence 5433, Ap
34	89	14.4	849	9	US-11-096-568A-21222 Sequence 21222, A
35	89	14.4	1107	9	US-11-087-099-132 Sequence 132, App
36	88	14.3	1976	9	US-11-072-512-1680 Sequence 1680, Ap
37	87	14.1	1250	9	US-11-096-568A-23080 Sequence 23080, A
38	86.5	14.0	615	9	US-11-096-568A-730 Sequence 730, App
39	86	14.0	791	9	US-11-096-568A-20676 Sequence 20676, A
40	86	14.0	2008	8	US-10-955-054A-150 Sequence 150, App
41	85.5	13.9	1479	9	US-11-096-568A-6605 Sequence 6605, Ap
42	85.5	13.9	2138	9	US-11-096-568A-11058 Sequence 11058, A
43	85	13.8	3599	12	US-11-080-991-39 Sequence 39, Appl
44	84.5	13.7	1287	9	US-11-096-568A-24773 Sequence 24773, A
45	84	13.6	362	7	US-10-991-285-134 Sequence 134, App

ALIGNMENTS

RESULT 1
US-11-096-568A-11809
; Sequence 11809, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11809
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(660)
; OTHER INFORMATION: Ceres Seq. ID no. 13657464
US-11-096-568A-11809

Alignment Scores:	1.97e-49	Length:	660
Pred. No.:	527.00	Matches:	94
Score:	79.8%	Conservative:	5
Best Local Similarity:	75.8%	Mismatches:	7
Query Match:	85.6%	Indels:	18


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; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-78459

Alignment Scores:
Pred. No.: 8,03e-34 Length: 366
Score: 385.00 Matches: 64
Percent Similarity: 65.5% Conservatives: 10
Best Local Similarity: 56.6% Mismatches: 29
Query Match: 62.5% Indels: 10
DB: 7 Gaps: 1

US-09-541-462B-2 (1-108) x US-10-932-182A-78459 (1-366)

Qy 5 MetAspValAspThrProSerGlyThrAsnSerGlyAlaGly-----18
Db 22 ATGGATGTTGATGAAGATGAATCGCAAAATATTTCGCAAAAGCTCAAAATCAAAGTGCGCCA 81
Qy 19 -----LysLysArgPheGluValLysTrpAsnAlaValAlaLeuTrpAla 34
Db 82 GTGGAACCAAAAGAGAGATTGAAATTAAGAAATGGACCCAGCTGGCGTTTGGTCA 141
Qy 35 TrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIle 54
Db 142 TGGGATATAGCTGTTGACAACTGTGCTATTGTCAGGACCATATATATGGAACCATGCGATT 201
Qy 55 GluCysGlnAlaAsnGlnAlaThrSerGluGluCysThrValAlaIleTrpGlyVal 74
Db 202 GAATGCCAGCCAAAGGCCATGACGACACTGTAATGAATGTGTAGCAGCTGGGGTGTG 261
Qy 75 CysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCys 94
Db 262 TGTAAATCAGCTTTCCATTTTGCACCTGTATTATTAATAATGGATCAAGACAGACGCGATGC 321
Qy 95 ProLeuAspAsnArgGluTrpGluPheGlnLysTyxGly 107
Db 322 CCATTAGTAACCAACCTTGGCAGTTAGCAAGATGCGGT 360

RESULT 6
US-10-932-182A-78459
; Sequence 78459, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78459
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-78459

Alignment Scores:
Pred. No.: 8,03e-34 Length: 366
Score: 385.00 Matches: 64
Percent Similarity: 65.5% Conservatives: 10
Best Local Similarity: 56.6% Mismatches: 29
Query Match: 62.5% Indels: 10
DB: 7 Gaps: 1

US-09-541-462B-2 (1-108) x US-10-932-182A-78459 (1-366)

Qy 5 MetAspValAspThrProSerGlyThrAsnSerGlyAlaGly-----18
Db 22 ATGGATGTTGATGAAGATGAATCGCAAAATATTTCGCAAAAGCTCAAAATCAAAGTGCGCCA 81

; Sequence 28569, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28569
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(348)
; OTHER INFORMATION: Ceres Seq. ID no. 3017472
US-11-096-568A-28569

Alignment Scores:
Pred. No.: 1.27e-46 Length: 348
Score: 499.00 Matches: 88
Percent Similarity: 86.1% Conservatives: 5
Best Local Similarity: 81.5% Mismatches: 13
Query Match: 81.0% Indels: 2
DB: 9 Gaps: 1

US-09-541-462B-2 (1-108) x US-11-096-568A-28569 (1-348)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 28 ATGGGTGAATCTCTCCATCTCCGTACCTTCA-----TCTGTCGAAGAACTCGAAA 81
Qy 21 ArgPheGluValLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 82 CGATTGTAATTAAGAGTGGAGTGTGTCGCTCTCTGCGCTTGGGCTATCGTTGTTGAT 141
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 142 AACTGGCAATTTGAGGAATACATCATGATCTCTGTTGATGATGCTAGCTAATCAA 201
Qy 61 AlaSerAlaThrSerGluCysThrValAlaIleTrpGlyValCysAsnHisAlaPheHis 80
Db 202 GCTAGTGCCACTAGTCAGGAATGCACTGTGCTTGGGGGGTTTGAACACACGCGCTTTCAC 261
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 262 TTCCACTGTATCAGCAGATGGCTCAAACTCGTCAAGTGTGTCCTAGATGTCCTGCGAG 321
Qy 101 TrpGluPheGlnLysTyxGlyHis 108
Db 322 TGGGAATTCAGAAATATGTCAC 345

RESULT 5
US-10-932-182A-78459
; Sequence 78459, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78459
; LENGTH: 366
; TYPE: DNA

```

```
QY 19 -----LysLysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAla 34
Db 82 GTGAAACCAAAGAGAGATTGAAATTAAGAAATGGACCCAGTGGCGTTTGGTCA 141
QY 35 TrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIle 54
Db 142 TGGGATATAGCTGTTGACACACTGCTATTGTCAGGAACCATATATATGGAACCATGCATT 201
QY 55 GluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyVal 74
Db 202 GAATGCCAGCAAGGCCATGACGACACTGATAATGAATGTTGTAGCAGCTGGGTGTC 261
QY 75 CysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCys 94
Db 262 TGTAAATCACCTTTCCATTTGCATGTTGATTAATAATGATCAAGACAGACGACGATGC 321
QY 95 ProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 322 CCATTAGTAACCAACCTTGGCAGTTAGCAAGATGCGGT 360
```

RESULT 7

```
US-10-932-182A-2279
; Sequence 2279, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2279
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2279
```

```
Alignment Scores:
Pred. No.: 2.25e-33 Length: 366
Score: 381.00 Matches: 62
Percent Similarity: 73.0% Conservative: 11
Best Local Similarity: 62.0% Mismatches: 23
Query Match: 61.9% Indels: 4
DB: 7 Gaps: 1
```

US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)

```
QY 8 AspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrp 27
Db 73 AATACACCGGTAGACACAAA-----AAAAAAGATTGAGATTAATAAATGG 120
QY 28 AsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsn 47
Db 121 ACACGGTGGCGTTCTGTCGTGGATATAGCCGTTGACAACTGTGCCATTGCGAANAAC 180
QY 48 HisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGlu 67
Db 181 CACATTATGGAACCATGCATCGAATGCCAGCGGAGGCTATGACCGACACAGATAACGAA 240
QY 68 CysThrValAlaTrpGlyValCysAsnHisAlaPheHisCysIleSerArgTrp 87
Db 241 TGTGTGGCAGATGGGGTGTGTTGTAATACGCTTTCCACTTGCATCATCAATAATGG 300
QY 88 LeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 301 ATCAAGACGAGATGTCATGCCGTTGGACAAACCAACCTTGGCAATTGGCAAGTGGCGGT 360
```

RESULT 8

```
US-10-932-182A-2279
; Sequence 2279, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2279
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2279
```

```
Alignment Scores:
Pred. No.: 2.25e-33 Length: 366
Score: 381.00 Matches: 62
Percent Similarity: 73.0% Conservative: 11
Best Local Similarity: 62.0% Mismatches: 23
Query Match: 61.9% Indels: 4
DB: 7 Gaps: 1
```

US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)

```
QY 8 AspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrp 27
Db 73 AATACACCGGTAGACACAAA-----AAAAAAGATTGAGATTAATAAATGG 120
QY 28 AsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsn 47
Db 121 ACACGGTGGCGTTCTGTCGTGGATATAGCCGTTGACAACTGTGCCATTGCGAANAAC 180
QY 48 HisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGlu 67
Db 181 CACATTATGGAACCATGCATCGAATGCCAGCGGAGGCTATGACCGACACAGATAACGAA 240
QY 68 CysThrValAlaTrpGlyValCysAsnHisAlaPheHisCysIleSerArgTrp 87
Db 241 TGTGTGGCAGATGGGGTGTGTTGTAATACGCTTTCCACTTGCATCATCAATAATGG 300
QY 88 LeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 301 ATCAAGACGAGATGTCATGCCGTTGGACAAACCAACCTTGGCAATTGGCAAGTGGCGGT 360
```

RESULT 9

```
US-10-821-234-554
; Sequence 554, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 554
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-554
```


Alignment Scores:

Pred. No.:	1,96e-23	Length:	342
Score:	292.00	Matches:	49
Percent Similarity:	64.9%	Conservative:	14
Best Local Similarity:	50.5%	Mismatches:	30
Query Match:	47.4%	Indels:	4
DB:	8	Gaps:	2

US-09-541-462B-2 (1-108) x US-10-821-234-554 (1-342)

Qy	11	SerGlyThrAsnSerClyAlaClyLysLysArgPheGluValLysLysTyrAsnAlaVal	30
Db	58	TCAGGCTCAAGTGGCGA---GGCGACAAGATGTTCCCTCAAGAAGTGGAAACGGCGTC	114
Qy	31	AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet	50
Db	115	GCCATGTGGAGCTGGACGTGGAGTGCATACGTGGCCATCTGCAGGGTCCAGGTGATG	174
Qy	51	AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal	70
Db	175	GATGCTGTCTTAGATGTCAAGCTGAAAC-----AAACAAGAGGACTGCTGTTGTG	225
Qy	71	AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr	90
Db	226	GTCGGGGAGATGTAACTCCTTCCCAACTGCTGCATGCCCTCGGTGGTGAACACAG	285
Qy	91	ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnIlystyrGly	107
Db	286	AAACAATCGTGGCCCTCTCTGGCAGCAGACATGGGTGGTCCAAAGAATCGGC	336

RESULT 10

US-11-128-061-5740
; Sequence 5740, Application US/11128061
; Publication NO. US20060003958A1
; GENERAL INFORMATION:-
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION

```

FILE REFERENCE: 039597-027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT FILING DATE: 2005-05-11
PRIORITY APPLICATION NUMBER: US 60/570,425
PRIORITY FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5740
LENGTH: 546
TYPE: DNA
ORGANISM: Cricetus griseus
FEATURE:
NAME/KEY: misc feature
LOCATION: (123)..(154)
OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-5740

```

Alignment Scores:		
Pred. No.:	1.07e-16	546
Score:	234.00	410
Percent Similarity:	56.7%	18
Best Local Similarity:	42.3%	38
Query Match:	38.0%	4
DB:	12	2
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-09-541-462B-2 (1-108) x US-11-128-061-5740 (1-546)

Qy		11	SerGlyThrAsnSerGlyAlaGlyIysLysArgPheGluValLysIleYsrTrpAsnAlaVal	30
Db		50	CGGGCTCCAAGTCGGGG--GGGCACAAGATGTTCCTCCCAAGAAGTGGAAACGCCGTA	106
Qy		31	AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet	50
Db		107	GCCATGTGGACCTGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTCCAGGTGATG	166
Qy		51	AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluCysThrVal	70
Db		167	GATGCCTGCCTCAGATGTCAAGCCGA AAC-----AACAAGAGAGCATGTGTGTGTG	217
Qy		71	AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr	90
Db		218	GTCTGGGGAGAAATGTAATCATCTCTTTCCAACTGCTGCATGTCTCTGTGGGTGAACAG	277
Qy		91	ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTryGly	107
Db		278	AACAATCGCTCTCTCTGTCAGCAGACATGGGTGGTCCAAAGAAATTGCC	328

RESULT 11

```

US-11-128-049-5740
: Publication 5740, Application US/11128049
: Sequence No. US20060010513A1
: GENERAL INFORMATION:
:
: APPLICANT: Melville, Mark W.
: APPLICANT: Charlebois, Timothy S.
: APPLICANT: Mounts, William M.
: APPLICANT: Hann, Louane E.
: APPLICANT: Sinacore, Martin S.
: APPLICANT: Leonard, Mark W.
: APPLICANT: Brown, Eugene L.
: APPLICANT: Miller, Christopher P.
: TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS
: TITLE OF INVENTION: MAKING AND USING SAME

```

```

1 FILE REFERENCE: 01997-027700
2
3 CURRENT APPLICATION NUMBER: US/11/128,
4
5 CURRENT FILING DATE: 2005-05-11
6
7 PRIOR APPLICATION NUMBER: US 60/570,421
8
9 PRIOR FILING DATE: 2004-05-11
10
11 NUMBER OF SEQ ID NOS: 7285
12
13 SOFTWARE: PatentIn version 3.3
14
15 SEQ ID NO 5740
16
17 LENGTH: 546
18
19 TYPE: DNA
20
21 ORGANISM: Cricetus griseus
22
23 FEATURES:
24
25 NAME/KEY: misc_feature
26
27 LOCATION: (123)..(154)
28
29 OTHER INFORMATION: n is a, c, g, or t
30
31 US-11-128-049-5740

```

Alignment Scores:	1.07e-16	Length:	546
Pred. No.:	234.00	Matches:	41
Score:	56.7%	Conservative:	18
Percent Similarity:	42.3%	Mismatches:	38
Best Local Similarity:	38.0%	Indels:	4
Query Match:	12	Gaps:	2
DB:			

Qy	11	SerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTyrTyrAsnAlaVal	30
Db	50	CGCGGCTCCAAGTCGGG---GGCGACAAGATGTTCTCCCTCAGAAGTGGAAACGCGGTA	106
Qy	31	AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet	50
Db	107	GCCATGTGGAGCTGGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTCCAGGTGATG	166
Qy	51	AspLeuCysIleGluCysGlnAlaAsnClnAlaSerAlaThrSerGluGluCysThrVal	70
Db	167	GATGCTGCTCCAGATGTCAAGCGCAAAAC-----AAACAAGAGACTGCTGTTGTG	217

Qy 71 AlaTrrpGlyValCysAsnHisAlaPheHisPheHisCysAlleserArgTrrpLeuLysThr 90
Db 218 GTCTGGGGAGAAATGTAATCATCTCTTCAACAAGTGTCTGTGGTGAACAG 277
Qy 91 ArgGlnValCysProLeuAspAsnArgGluTrrpGluPheGlnLysTyrGly 107
Db 278 AACAAATCGCTGCTCTCTCCAGCAGGACTGGGTGTCCTCAAGAAATTGGC 328

RESULT 12
US-11-128-061-2098
; Sequence 2098, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2098
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (123)..(154)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (547)..(568)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-2098

Alignment Scores:
Pred. No.: 1,15e-16 Length: 579
Score: 234.00 Matches: 41
Percent Similarity: 56.7% Conservative: 14
Best Local Similarity: 42.3% Mismatches: 38
Query Match: 38.0% Indels: 4
DB: 12 Gaps: 2

US-09-541-462B-2 (1-108) x US-11-128-061-2098 (1-579)

Qy 11 SerGlyThrAsnSerGlyAlaGlyLysArgPheGluValLysLysTrrpAsnAlaVal 30
Db 50 GCGGGCTCCAAGTCGGG---GGCGACAAGATGTTCTCCCTCAAGAAGTGGACCGGTA 106
Qy 31 AlaLeuTrrpAlaTrrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 107 GCCATGTGGAGCTGGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTCCAGGTGATG 166
Qy 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
Db 167 GATCGCTCCCTCAGATGTCAGGCCGAAAC-----AAACAAGAGGACTGTGTGTG 217
Qy 71 AlaTrrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrrpLeuLysThr 90
Db 218 GTCTGGGGAGAAATGTAATCATCTCTTCAACAAGTGTCTGTGGTGAACAG 277
Qy 91 ArgGlnValCysProLeuAspAsnArgGluTrrpGluPheGlnLysTyrGly 107
Db 278 AACAAATCGCTGCTCTCTCCAGCAGGACTGGGTGTCCTCAAGAAATTGGC 328

Db 278 AACAAATCGCTGCTCTCTCTCCAGCAGGACTGGGTGTCCTCAAGAAATTGGC 328

RESULT 13
US-11-128-049-2098
; Sequence 2098, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING SAME
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2098
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (123)..(154)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (547)..(568)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-2098

Alignment Scores:
Pred. No.: 1,15e-16 Length: 579
Score: 234.00 Matches: 41
Percent Similarity: 56.7% Conservative: 14
Best Local Similarity: 42.3% Mismatches: 38
Query Match: 38.0% Indels: 4
DB: 12 Gaps: 2

US-09-541-462B-2 (1-108) x US-11-128-049-2098 (1-579)

Qy 11 SerGlyThrAsnSerGlyAlaGlyLysArgPheGluValLysLysTrrpAsnAlaVal 30
Db 50 GCGGGCTCCAAGTCGGG---GGCGACAAGATGTTCTCCCTCAAGAAGTGGACCGGTA 106
Qy 31 AlaLeuTrrpAlaTrrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 107 GCCATGTGGAGCTGGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTCCAGGTGATG 166
Qy 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
Db 167 GATCGCTCCCTCAGATGTCAGGCCGAAAC-----AAACAAGAGGACTGTGTGTG 217
Qy 71 AlaTrrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrrpLeuLysThr 90
Db 218 GTCTGGGGAGAAATGTAATCATCTCTTCAACAAGTGTCTGTGGTGAACAG 277
Qy 91 ArgGlnValCysProLeuAspAsnArgGluTrrpGluPheGlnLysTyrGly 107
Db 278 AACAAATCGCTGCTCTCTCCAGCAGGACTGGGTGTCCTCAAGAAATTGGC 328

RESULT 14
US-09-978-360A-4
; Sequence 4, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:

```

; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.USA.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 4
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..438
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 612..617
; FEATURE:
; NAME/KEY: polyA site
; LOCATION: 632..648
; US-09-978-360A-4

Alignment Scores:
Pred. No.: 1.06e-14 Length: 648
Score: 217.00 Matches: 43
Percent Similarity: 44.5% Conservative: 18
Best Local Similarity: 31.4% Mismatches: 40
Query Match: 35.2% Indels: 36
DB: 5 Gaps: 3

US-09-541-462B-2 (1-108) x US-09-978-360A-4 (1-648)

Qy 2 AlaalaMetaspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArg 21
Db 49 GCGCGGAGTGTGTCGTTTATACCTTCGCGCGGACGCCGCGCTGCCAACGGAAG 108
Qy 22 PheGlu-----ValLysLysTrpAsnAlaValalaLeuTrp 33
Db 109 GCGGAGAGCGAGTTTCGTCATGTTGGCCAGGCCCATTTGAGATCTTTGAAGATATCTCA 168
Qy 24 -----ValLysLysTrpAsnAlaValalaLeuTrp 33
Db 169 ACGTGAGGCTCTGCTGCATGAAGTGAAGTAAAGTCTGGAACGCGTGGCCACTTGG 228
Qy 34 AlaTrpAspIleValValaspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCys 53
Db 229 CTCCTGGTGCCCAACGATGAGAACTGTGGCATCTGCAGGATGGCATTTAAACGGATGCTGC 288

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Qy 54 IleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGly 73
Db 289 CCTGACTGCAAG-----GTGCGCGGCGACGACTGCCCGCTGGTGTGGGC 333
Qy 74 ValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnVal 93
Db 334 CAGTGCTCCCACTGCTTCCACATGTCATCTCAAGTGGTGGTGCACGACGACAGTG 393
Qy 94 -----CysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 394 CAGCAGCACTGCCCATGTGCCCGCAGGAATGGAAGTTCAAGGAGTGAGGC 444

RESULT 15
US-11-057-484A-14
; Sequence 14, Application US/11057484A
; Publication No. US20060029931A1
; GENERAL INFORMATION:
; APPLICANT: Finkel, Terri H.
; APPLICANT: Yin, JiYi
; TITLE OF INVENTION: Cellular Genes Regulated by HIV-1
; FILE REFERENCE: CHOP.0146CIP
; CURRENT APPLICATION NUMBER: US/11/057,484A
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 10/368,803
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/358,495
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: n = A, C, G or T
; US-11-057-484A-14

Alignment Scores:
Pred. No.: 1.15e-14 Length: 450
Score: 215.00 Matches: 41
Percent Similarity: 53.6% Conservative: 11
Best Local Similarity: 42.3% Mismatches: 23
Query Match: 34.9% Indels: 23
DB: 9 Gaps: 2

US-09-541-462B-2 (1-108) x US-11-057-484A-14 (1-450)

Qy 11 SerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaVal 30
Db 54 TCAGGCTCCAGTCCGGA---GGCGACAGATGTTCTCCCTCAAGAGTGGACCGCGTG 110
Qy 31 AlaLeuTrpAlaTrpAspIleValValaspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 111 GCCATGTGGAGCTGGGACGCGTGGAGTACGTCGCGCCATCTGCAGGT----- 160
Qy 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
Db 161 -----CCAGTG 166
Qy 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
Db 167 GTCGTGGGAGAGATGTAATCATCTCTTCCAACTGCTGCAATGCTCCCTGGTGGTGAACAG 226
Qy 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 227 AACAACTGNTGCCCTCTCTGCCAGCAGGACTGGTGGTCCAAAGATCGGC 277

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Search completed: March 11, 2006, 08:43:57
Job time : 352 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2006, 08:13:49 ; Search time 134 Seconds
(without alignments)
1432.662 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 616
Sequence: 1 MAAMDVTPSGTNGAGKK.....KTRQVCLDNREWFQYKXH 108

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-HOST=abes05h -USER=US09541462 @CGN 1 1 193 @runat 10032006 080729 22008
-NCPU=6 -ICPU=3 -NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:**
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:**
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:**
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:**
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:**
- 6: /cgn2_6/ptodata/1/ina/PCUS COMB.seq:**
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:**
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:**
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	616	100.0	504	3	US-09-914-324A-5
3	616	100.0	507	3	US-09-949-016-4940
4	616	100.0	508	3	US-09-914-324A-3
5	501.5	81.4	3208	3	US-09-780-016-27
6	501.5	81.4	3208	3	US-10-214-811-27
7	501.5	81.4	3208	3	US-10-766-074-27
8	479	77.8	411	3	US-09-640-211A-1731
9	400.5	65.0	490	3	US-09-270-767-26812

c	10	400.5	65.0	1101	3	US-09-270-767-11265	Sequence 11265, A
	11	394	64.0	402	3	US-09-513-999C-10371	Sequence 10371, A
	12	394	64.0	463	3	US-09-621-976-15180	Sequence 15180, A
	13	385	62.5	480	3	US-09-914-324A-4	Sequence 4, Appli
	14	375.5	61.0	357	3	US-09-248-796A-5495	Sequence 5495, Ap
	15	287	46.6	342	3	US-09-826-312A-7	Sequence 7, Appli
	16	287	46.6	342	3	US-09-542-497A-7	Sequence 7, Appli
	17	287	46.6	342	3	US-10-108-767-7	Sequence 7, Appli
	18	262.5	42.6	301	3	US-09-313-294A-492	Sequence 492, App
	19	217	35.2	648	3	US-09-599-360B-27	Sequence 27, Appl
	20	200.5	32.5	534	3	US-09-621-976-1817	Sequence 1817, Ap
	21	198	32.1	671	3	US-09-621-976-1854	Sequence 1854, Ap
	22	197.5	32.1	539	3	US-09-621-976-2051	Sequence 2051, Ap
	23	191	31.0	654	3	US-09-621-976-1945	Sequence 1945, Ap
	24	175	28.4	25274	3	US-09-949-016-16682	Sequence 16682, A
	25	173	28.1	585	3	US-09-270-767-10788	Sequence 10788, A
	26	150.5	24.4	439	3	US-09-799-451-286	Sequence 286, App
	27	146	23.7	170	3	US-09-270-767-26253	Sequence 26253, A
	28	137.5	22.3	2135	3	US-10-104-047-459	Sequence 459, App
	29	91	14.8	940	3	US-09-023-655-667	Sequence 667, App
	30	91	14.8	1839	3	US-09-828-303-10	Sequence 10, Appl
	31	90	14.6	872	3	US-09-774-528-304	Sequence 304, App
	32	90	14.6	872	3	US-10-120-988-304	Sequence 304, App
	33	90	14.6	893	3	US-09-949-016-4980	Sequence 4980, Ap
	34	90	14.6	1690	3	US-09-828-303-2	Sequence 2, Appli
	35	90	14.6	3140	3	US-09-774-528-255	Sequence 255, App
	36	90	14.6	3140	3	US-10-120-988-255	Sequence 255, App
	37	90	14.6	8438	2	US-07-945-283-1	Sequence 1, Appli
	38	88	14.3	1183	3	US-09-799-451-763	Sequence 763, App
	39	88	14.3	1976	3	US-10-104-047-1680	Sequence 1680, Ap
	40	86	14.0	363	3	US-09-640-211A-1319	Sequence 1319, Ap
	41	86	14.0	1267	3	US-09-949-016-378	Sequence 378, App
	42	86	14.0	1267	3	US-09-949-016-2914	Sequence 2914, Ap
	43	85.5	13.9	3304	3	US-09-799-451-220	Sequence 220, App
	44	85	13.8	1621	3	US-03-023-655-20	Sequence 20, Appl
	45	85	13.8	1995	3	US-09-949-016-3134	Sequence 3134, Ap

ALIGNMENTS

RESULT 1

US-09-513-999C-3894
; Sequence 3894, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3894
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29...352
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 401
; OTHER INFORMATION: r-a or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 404
; OTHER INFORMATION: m-a or c
US-09-513-999C-3894

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Pred. No.: 1.48e-66 Length: 482
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-513-999C-3894 (1-482)
QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 29 ATGGCGCGCGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 88
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 89 CGCTTTGAAGTGAAGAGTGGATGCAAGTAGCCCTCTGGGCGCTGGGATATTGGTTGAT 148
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 149 AACTGTGCCATCTGCAGGAACCAATATGATGATGATGATGATGATGATGATGATGAT 208
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
Db 209 GCGTCCGCTACTTCCAGAGAGTGTACTGTGCGATGGGAGTGTGTAACCATGCTTTTCAC 268
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 269 TTCCATGCAATCTCTCGCTGGCTCAAAACAGCAGCAGGTGTGTCATTTGGACACAGAG 328
QY 101 TrpGluPheGlnLysTyrGlyHis 108
Db 329 TGGGAATTCCAAAAGTATGGGCAC 352

RESULT 2
US-09-914-324A-5
; Sequence 5, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kanura, Takumi
; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(344)
; OTHER INFORMATION: Rbx1
US-09-914-324A-5

Alignment Scores:
Pred. No.: 1.57e-66 Length: 504
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-914-324A-5 (1-504)
QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 7 ATGGCGCGCGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 66
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db 67 CGCTTTGAAGTGAAGAGTGGATGCAAGTAGCCCTCTGGGCGCTGGGATATTGGTTGAT 126
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 127 AACTGTGCCATCTGCAGGAACCAATATGATGATGATGATGATGATGATGATGATGAT 186

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QY 61 AlaSerAlaThrSerGluGluCysThrValAlaLysThrGlyValCysAsnHisAlaPheHis 80
Db 187 GCGTCCGCTACTTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
QY 81 PheHisCysIleSerArgTyrLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 247 TTCACATGCACTCTCCGCTGGCTTAAACACACGACAGGTGTGTCTCATTTGGACACAGAGAG 306

QY 101 TrpGluPheGlnLysTyrGlyHis 108
Db 307 TGGGAATTCAAAAGTAGTGGGCAC 330

RESULT 4

US-09-914-324A-3
; Sequence 3, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; TITLE OF INVENTION: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(333)
; OTHER INFORMATION: Rbx1

US-09-914-324A-3

Alignment Scores:
Pred. No.: 1,58e-66 Length: 508
Score: 616.00 Matches: 108
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-914-324A-3 (1-508)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
Db 7 ATGCGCGCAGCGATGTGGATGTGATACCCGCGCGCACCAACAGCGCGCGGCAAGAG 66
QY 21 ArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaLysValValValAsp 40
Db 67 CGCTTTGAGTGAAGTGAAGTGCAGTAGCCCTCTGGGCTGGGATATTGGTTGAT 126

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 127 AACTGTGCCATCTCCAGGAACCAACATATGATCTTTGCATAGATGCTCAAGCTAACAG 186

QY 61 AlaSerAlaThrSerGluGluCysThrValAlaLysThrArgGlnValCysAsnHisAlaPheHis 80
Db 187 GCGTCCGCTACTTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCAC 246

QY 81 PheHisCysIleSerArgTyrLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 247 TTCACATGCACTCTCCGCTGGCTTAAACACACGACAGGTGTGTCTCATTTGGACACAGAGAG 306

QY 101 TrpGluPheGlnLysTyrGlyHis 108

Db 307 TGGGAATTCAAAAGTAGTGGGCAC 330

RESULT 5

US-09-780-016-27
; Sequence 27, Application US/09780016
; Patent No. 6509456
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6509456el Human Proteases and
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/09/780,016
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-780-016-27

Alignment Scores:
Pred. No.: 2.1e-51 Length: 3208
Score: 501.50 Matches: 88
Percent Similarity: 95.7% Conservative: 1
Best Local Similarity: 94.6% Mismatches: 1
Query Match: 81.4% Indels: 3
DB: 3 Gaps: 1

US-09-541-462B-2 (1-108) x US-09-780-016-27 (1-3208)

QY 16 GlyValaGlyLysLysArgPheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaLys 35
Db 2752 GGAGCATATAAAAAA-----AAAAATGGAATCAGTAGCCCTCTGGGCTGG 2802
QY 36 AspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGlu 55
Db 2803 GATATTGTGTGTGTATTAATGTGTCATCTGCAGAACACACATTATGGATCTTTGCATAGAA 2862
QY 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaLysGlyValCys 75
Db 2863 TGTCAAGCTAACCCAGCGCTCCGCTACTTTCAGAGAGTGTACTGTCCGATGGGAGTCTGT 2922

QY 76 AsnHisAlaPheHisPheHisCysIleSerArgTyrLeuLysThrArgGlnValCysPro 95
Db 2923 AACCATGCTTTTTCATCTCCATCTCCATCTCCGCTGGCTCAAAACACGACAGGTGTGTGCCA 2982

QY 96 LeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108
Db 2983 TTGCACACAGAGAGTGGGAATTCAAAAGTAGTGGGCAC 3021

RESULT 6

US-10-214-811-27
; Sequence 27, Application US/10214811
; Patent No. 6743621
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743621el Human Proteases and

```

; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/10/214,811
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-214-811-27

Alignment Scores:
Pred. No.: 2,1e-51 Length: 3208
Score: 501.50 Matches: 88
Percent Similarity: 95.7% Conservative: 1
Best Local Similarity: 94.6% Mismatches: 1
Query Match: 81.4% Indels: 3
DB: Gaps: 1

US-09-541-462B-2 (1-108) x US-10-214-811-27 (1-3208)
QY 16 GlyAlaGlyLysIysArgPheGluValLysLysTTPAsnAlaValAlaLeuTTPAlaTTP 35
Db 2752 GGAGCATATAAAAAA-----AAAAATGGAATGCAGTAGCCCTCTGGGCTGG 2802
QY 36 AspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGlu 55
Db 2803 GATATTGTGTTGATTAACCTGTCATCTGCAGAACACACATTATGATCTTTGCATAGAA 2862
QY 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTTPGlyValCys 75
Db 2863 TGTCAAGCTAACAGGCGTCCGCTACTTCAAGAGAGTGTACTGTGCGATGGGAGTCTGT 2922
QY 76 AsnHisAlaPheHisPheHisCysIleSerArgTTPLeuLysThrArgGlnValCysPro 95
Db 2923 AACCATGCTTTTCACTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCA 2982
QY 96 LeuAspAsnArgGluTTPGluPheGlnLysTyrGlyHis 108
Db 2983 TTGGACACAGAGAGTGGGAATTCCTCAAAAGTATGGGCAC 3021

RESULT 7
US-10-766-074-27
; Sequence 27, Application US/10766074
; Patent No. 6881563
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/10/766,074
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/10/214,811
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208

; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/10/214,811
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208

; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-766-074-27

Alignment Scores:
Pred. No.: 2,1e-51 Length: 3208
Score: 501.50 Matches: 88
Percent Similarity: 95.7% Conservative: 1
Best Local Similarity: 94.6% Mismatches: 1
Query Match: 81.4% Indels: 3
DB: Gaps: 1

US-09-541-462B-2 (1-108) x US-10-214-811-27 (1-3208)
QY 16 GlyAlaGlyLysIysArgPheGluValLysLysTTPAsnAlaValAlaLeuTTPAlaTTP 35
Db 2752 GGAGCATATAAAAAA-----AAAAATGGAATGCAGTAGCCCTCTGGGCTGG 2802
QY 36 AspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGlu 55
Db 2803 GATATTGTGTTGATTAACCTGTCATCTGCAGAACACACATTATGATCTTTGCATAGAA 2862
QY 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTTPGlyValCys 75
Db 2863 TGTCAAGCTAACAGGCGTCCGCTACTTCAAGAGAGTGTACTGTGCGATGGGAGTCTGT 2922
QY 76 AsnHisAlaPheHisPheHisCysIleSerArgTTPLeuLysThrArgGlnValCysPro 95
Db 2923 AACCATGCTTTTCACTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCA 2982
QY 96 LeuAspAsnArgGluTTPGluPheGlnLysTyrGlyHis 108
Db 2983 TTGGACACAGAGAGTGGGAATTCCTCAAAAGTATGGGCAC 3021

RESULT 8
US-09-640-211A-1731
; Sequence 1731, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1731
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Pinus radiata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(411)
; OTHER INFORMATION: n = A,T,C or G
; US-09-640-211A-1731

Alignment Scores:
Pred. No.: 7,79e-50 Length: 411
Score: 479.00 Matches: 90
Percent Similarity: 85.0% Conservative: 6
Best Local Similarity: 79.6% Mismatches: 4
Query Match: 77.8% Indels: 13
DB: Gaps: 3

US-09-541-462B-2 (1-108) x US-09-640-211A-1731 (1-411)
QY 3 AlaAlaMetAspValAsp-----ThrProSer-----GlyThrAsnSerGlyAla 17
Db 74 GCTTCAACACAGACATAGATATGATTCGCGTGCCTCTGGCGAGGTTCCAGCTCTCAAGCG 133

```



```
/ FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 20
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 38
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 79
; OTHER INFORMATION: n=a, g, c o r t
; US-09-513-999C-10371

Alignment Scores:
Pred. No.:      2,05e-39          Length:      402
Score:           394.00         Matches:       76
Percent Similarity:   73.1%     Conservative:    0
Best Local Similarity: 73.1%     Mismatches:    2
Query Match:        64.0%       Indels:       27
DB:                3              Gaps:        1

US-09-541-462B-2 (1-108) x US-09-513-999C-10371 (1-402)

QY      5 MetAspValAepThrProSerGlyThraSenSerGlyAlaGlyLysLysArgPheGluVal 24
| | | | |
Db      40 ATGGATGTGGATAFACCCCGAGCGGCCAACACAGCGCGCGNGCAAGAAGCGCTTTGAAGTG 99
| | | | |
QY      25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIle 44
| | | | |
Db      100 AAAAAAGGC----- 107
| | | | |

QY      45 CysArgAsnHisIleMetAspLeuCystileGluCysGlnAlaAsnGlnAlaSerAlaThr 64
| | | | |
Db      108 -----ATAGTAATGTCAAGTCAACTAAACCATGCTTTTCACATTCCACTGCATC 140
| | | | |

QY      65 SerGluGluCyThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIle 84
| | | | |
Db      141 TCAGAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACATTCCACTGCATC 200
| | | | |

QY      85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGln 104
| | | | |
Db      201 TCTCGCTGGCTCAAACAACACGACAGGTGTGTCCATTGGACAACACAGAGAGTGGGAATTC 260
| | | | |

QY      105 LysTyrrGlyHis 108
| | | | |
Db      261 AAGTAGTGGGCAC 272

RESULT 12
US-09-621-976-15180
; Sequence 15180, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15180
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 74
; OTHER INFORMATION: n=a, g, c o r t
; US-09-621-976--15180

Alignment Scores:
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QY 5 MetAspValAspThrProSerGlyThrAsnSerGlyAlaGly----- 18
DB 25 ATGGATGTTGATGAAGATGAATCGCAAAATATTCGCAAAAGCTCAAAACCAAGTGCGCCA 84
QY 19 -----LysLeuArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAla 34
DB 85 GTGGAAACCAAAAGAGAGATTGAAATTGAAGAAATGACCGCAGTGGCGTTTGGTCA 144
QY 35 TrpAspIleValAlaAsnAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIle 54
DB 145 TGGGATATAGCTGTTGCAACACTGTCTATTTCAGAGAACCATATAATGGAACCATGCATT 204
QY 55 GluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyVal 74
DB 205 GAATGCCAGCCAAAGCCATGACGACACATGATAATGAATGTAGCAGCCCTGGGGTGC 264
QY 75 CysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCys 94
DB 265 TGTATACAGCTTTCCATTTCACCTGTTATTAATTAATGATCAAGAACAGACGATGC 324
QY 95 ProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107
DB 325 CCATTAGATAACCAACCTTGGCAGTTAGCAAGATCGCGT 363
RESULT 14
US-09-248-796A-5495
; Sequence 5495, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5495
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-5495
Alignment Scores:
Pred. No.: 3,26e-37 Length: 357
Score: 375.50 Matches: 62
Percent Similarity: 73.3% Conservative: 12
Best Local Similarity: 61.4% Mismatches: 26
Query Match: 61.0% Indels: 1
DB: 3 Gaps: 1
US-09-541-462B-2 (1-108) x US-09-248-796A-5495 (1-357)
QY 9 ThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsn 28
DB 52 ACAACAGAACCAACATCAAAACCATCATCAAAACCAAGATTGAAGTGAAGAAATGACA 111
QY 29 AlaValAlaLeuTrpAlaTrpAspIleValAlaAspAsnCysAlaIleCysArgAsnHis 48
DB 112 GCGGTAGGTTTGGTTCATGGATATGCAAAATGCAAAATGTCGCAATTTGTAGAATCAT 171
QY 49 IleMetAspLeuCysIleGluCysGlnAlaAsn---GlnAlaSerAlaThrSerGluGlu 67
DB 172 TTAATGGAACCATGATTGTAATGCAACCAAAATGCTATGGGTAATATTTCTTCAGAAAG 231
QY 68 CysThrValAlaTrpGlyValCysAsnHisAlaPheHisCysIleSerArgTrp 87
DB 232 TGTATTCCTGCTGGGAGATGTAATCATGTCATTTCATTACATTTGATAGAAATGG 291
QY 88 LeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107

DB 292 TTGAACCAAGAAATGCAATGCTCCCTTGGATAGTACTAATTGCACTTATCAAAAAATTGGGT 351
QY 108 His 108
DB 352 AAT 354
RESULT 15
US-09-826-312A-7
; Sequence 7, Application US/09826312A
; Patent No. 6737244
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: 021044-007010US
; CURRENT APPLICATION NUMBER: US/09/826,312A
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: RING finger protein ROC2
US-09-826-312A-7
Alignment Scores:
Pred. No.: 2,24e-26 Length: 342
Score: 287.00 Matches: 48
Percent Similarity: 63.9% Conservative: 14
Best Local Similarity: 49.5% Mismatches: 31
Query Match: 46.6% Indels: 4
DB: 3 Gaps: 2
US-09-541-462B-2 (1-108) x US-09-826-312A-7 (1-342)
QY 11 SerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaVal 30
DB 58 TCAGGCTCAACGTCGGA---GGCGACAAGATGTTCTCCCTCAAGAAGTGGAAACCCGGTG 114
QY 31 AlaLeuTrpAlaTrpAspIleValAlaAspAsnCysAlaIleCysArgAsnHisIleMet 50
DB 115 GCCATGTGGAGCTGGGACGTGGAGTGCATACGTGCGCCATCTGCAGGGTCCAGGTGATG 174
QY 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
DB 175 GATGCCCTGTCTTAGATGTCAAGCTGAAAC-----AAACAAGAGGACTGTGTGTG 225
QY 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
DB 226 GTCTGGGAGAAATGTAATCATTTCTTCCAACTGCTGCATGTCCTGTGGTGGTGAACAG 285
QY 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107
DB 286 AACAAATCGCTGCCCTCTCTCTGCCAGCAGGACTGGGTGGTCCCAAGAATCGGC 336
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Job time : 137 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 14:30:51 ; Search time 297.184 Seconds
(without alignments)
2538.786 Million cell updates/sec

Title: US-09-541-462B-1
Perfect score: 327
Sequence: 1 atggcgagcgatgatgt.....tccaaagtatgggcactag 327

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 7673375 seqs, 1153648444 residues

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	7.6	25	12	US-11-121-849-188861 Sequence 188861,
2	25	7.6	25	12	US-11-121-849-188862 Sequence 188862,
3	25	7.6	25	12	US-11-121-849-188863 Sequence 188863,
4	25	7.6	25	12	US-11-121-849-188864 Sequence 188864,
5	25	7.6	25	12	US-11-121-849-188865 Sequence 188865,
6	25	7.6	25	12	US-11-121-849-188866 Sequence 188866,
7	25	7.6	25	12	US-11-121-849-188867 Sequence 188867,
8	23	7.0	23	12	US-11-090-617-351 Sequence 351, App
9	19	5.8	19	10	US-11-101-244-692822 Sequence 692822,
10	19	5.8	19	10	US-11-101-244-692823 Sequence 692823,
11	19	5.8	19	10	US-11-101-244-692824 Sequence 692824,
12	19	5.8	19	10	US-11-101-244-692826 Sequence 692826,
13	19	5.8	19	10	US-11-101-244-692827 Sequence 692827,
14	19	5.8	19	10	US-11-101-244-692829 Sequence 692829,
15	19	5.8	19	10	US-11-101-244-692830 Sequence 692830,
16	19	5.8	19	10	US-11-101-244-692831 Sequence 692831,
17	19	5.8	19	10	US-11-101-244-692832 Sequence 692832,
18	19	5.8	19	10	US-11-101-244-692833 Sequence 692833,
19	19	5.8	19	10	US-11-101-244-692835 Sequence 692835,
20	19	5.8	19	10	US-11-101-244-692836 Sequence 692836,

21	19	5.8	19	10	US-11-101-244-692837	Sequence 692837,
22	19	5.8	19	10	US-11-101-244-692840	Sequence 692840,
23	19	5.8	19	10	US-11-101-244-692841	Sequence 692841,
24	19	5.8	19	10	US-11-101-244-692842	Sequence 692842,
25	19	5.8	19	10	US-11-101-244-692843	Sequence 692843,
26	19	5.8	19	10	US-11-101-244-692844	Sequence 692844,
27	19	5.8	19	10	US-11-101-244-692845	Sequence 692845,
28	19	5.8	19	10	US-11-101-244-692846	Sequence 692846,
29	19	5.8	19	10	US-11-101-244-692848	Sequence 692848,
30	19	5.8	19	10	US-11-101-244-692849	Sequence 692849,
31	19	5.8	19	10	US-11-101-244-692850	Sequence 692850,
32	19	5.8	19	10	US-11-101-244-692852	Sequence 692852,
33	19	5.8	19	11	US-11-083-784-692822	Sequence 692822,
34	19	5.8	19	11	US-11-083-784-692823	Sequence 692823,
35	19	5.8	19	11	US-11-083-784-692824	Sequence 692824,
36	19	5.8	19	11	US-11-083-784-692826	Sequence 692826,
37	19	5.8	19	11	US-11-083-784-692827	Sequence 692827,
38	19	5.8	19	11	US-11-083-784-692829	Sequence 692829,
39	19	5.8	19	11	US-11-083-784-692830	Sequence 692830,
40	19	5.8	19	11	US-11-083-784-692831	Sequence 692831,
41	19	5.8	19	11	US-11-083-784-692832	Sequence 692832,
42	19	5.8	19	11	US-11-083-784-692833	Sequence 692833,
43	19	5.8	19	11	US-11-083-784-692835	Sequence 692835,
44	19	5.8	19	11	US-11-083-784-692836	Sequence 692836,
45	19	5.8	19	11	US-11-083-784-692837	Sequence 692837,

ALIGNMENTS

RESULT 1
US-11-121-849-188861
; Sequence 188861, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188861
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-188861

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 AGCGTCCGCTACTTTCAGAGAGTG 203

Db 1 AGCGTCCGCTACTTTCAGAGAGTG 25

RESULT 2

US-11-121-849-188862
; Sequence 188862, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03

```
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-188862
```

```
Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 193 TCAGAGAGTGTTACTCGCATGGG 217
Db 1 TCAGAGAGTGTTACTCGCATGGG 25
```

RESULT 3

```
US-11-121-849-188863
; Sequence 188863, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
```

```
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188863
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
```

```
US-11-121-849-188863
```

```
Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 246 CTGCATCTCTCGTGGCTCAAAACA 270
Db 1 CTGCATCTCTCGTGGCTCAAAACA 25
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RESULT 4

```
US-11-121-849-188864
; Sequence 188864, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
```

```
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188864
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
```

```
US-11-121-849-188864
```

```
Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 255 TCGCTGGCTCAAAACACGACGAGTG 279
```

```
Db 1 TCGCTGGCTCAAAACACGACGAGTG 25
```

RESULT 5

```
US-11-121-849-188865
; Sequence 188865, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
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; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188865
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
```

```
US-11-121-849-188865
```

```
Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 269 CACGACAGGTGTGTCCATTGGACAA 293
Db 1 CACGACAGGTGTGTCCATTGGACAA 25
```

RESULT 6

```
US-11-121-849-188866
; Sequence 188866, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
```

```
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188866
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
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US-11-121-849-188866
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Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 289 GACACACAGAGTGGGAATTCCTCAA 313
Db 1 GACACACAGAGTGGGAATTCCTCAA 25
```

RESULT 7

```
US-11-121-849-188867
; Sequence 188867, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
```

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; FILE REFERENCE: 3684.1
```

; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188867
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-188867

Query Match 7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 GGGAAATCCAAAGATATGGGCACTA 326
|||||
Db 1 GGGAAATCCAAAGATATGGGCACTA 25

RESULT 8

US-11-090-617-351
; Sequence 351, Application US/11/090617
; Publication No. US20060024692A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Daigo, Yataro
; APPLICANT: Nakatsuru, Shuichi
; TITLE OF INVENTION: METHOD FOR DIAGNOSING NON-SMALL CELL LUNG CANCERS
; FILE REFERENCE: 082368-003500US
; CURRENT APPLICATION NUMBER: US/11/090,617
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: PCT/JP04/04075
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: PCT/JP03/12072
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: US 60/555,757
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/466,100
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/451,374
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/414,673
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 706
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 351
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificially synthesized primer sequence for RT-PCR
US-11-090-617-351

Query Match 7.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GTGAAAAAGTGGAAATGCAGTAGC 92
|||||
Db 1 GTGAAAAAGTGGAAATGCAGTAGC 23

RESULT 9

US-11-101-244-692822
; Sequence 692822, Application US/11/101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692822
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-692822

Query Match 5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.7;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GCAAGAGCGCTTTGAAGT 71
|||||
Db 1 GCAAGAGCGCTTTGAAGT 19

RESULT 10

US-11-101-244-692823
; Sequence 692823, Application US/11/101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692823
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-692823

Query Match 5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.7;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 57 GAAGCGCTTTGAAGTGAAG 75
|||||
Db 1 GAAGCGCTTTGAAGTGAAG 19

RESULT 11

US-11-101-244-692824
; Sequence 692824, Application US/11/101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692824
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-692824

Query Match      5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 63.2%; Pred. No. 1.7;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 104 GGGATATTGTGTTGATAA 122
|||||:|:|:|:|:|:|
Db 1 GGGAAUUGUGGUGAUA 19

RESULT 12
US-11-101-244-692826
; Sequence 692826, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692826
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-692826

Query Match      5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.7;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 55 AAGAAGCGCTTTGAAGTGA 73
|||||:|:|:|:|:|:|
Db 1 AAGAAGCGCUUGAAGUA 19

RESULT 13
US-11-101-244-692827
; Sequence 692827, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

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; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692827
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-692827

Query Match      5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 291 CAACAGAGAGTGGGAATTC 309
|||||:|:|:|:|:|:|
Db 1 CAACAGAGAGUGGAAUUC 19

RESULT 14
US-11-101-244-692829
; Sequence 692829, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692829
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-692829

Query Match      5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 1.7;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 137 GGAACCAACATATGATCT 155
|||||:|:|:|:|:|:|
Db 1 GGAACCACAUAUGGAUCU 19

RESULT 15
US-11-101-244-692830
; Sequence 692830, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

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; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692830
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-692830

Query Match      5.8%; Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      134 GCAGGAACCACTTATGGA 152
        |||||
Db       1 GCAGGAACCAUUGGA 19

Search completed: March 8, 2006, 14:44:48
Job time : 297.184 secs
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QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAACAGAG 300
Db 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAACAGAG 319
QY 301 TGGGAATTCCAAAGTATGGCACTAG 327
Db 320 TGGGAATTCCAAAGTATGGCACTAG 346

RESULT 2

US-10-085-783A-43377
; Sequence 43377, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43377
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-43377

Query Match 100.0%; Score 327; DB 7; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.8e-173; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 0;
QY 1 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 20 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
QY 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATGTGGTTGAT 120
Db 80 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATGTGGTTGAT 139
QY 121 AACTGTGCCATCTGCAGGAACCACTATTATGGATCTTTTGCATAGAAATGCTCAAGCTAACCCAG 180
Db 140 AACTGTGCCATCTGCAGGAACCACTATTATGGATCTTTTGCATAGAAATGCTCAAGCTAACCCAG 199
QY 181 GCGTCCGCTACTTTCAGAAAGTGTACTGTCCGATGGGGAGTCTGTAAACCATGCTTTTTCAC 240
Db 200 GCGTCCGCTACTTTCAGAAAGTGTACTGTCCGATGGGGAGTCTGTAAACCATGCTTTTTCAC 259
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAACAGAG 300
Db 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAACAGAG 319
QY 301 TGGGAATTCCAAAGTATGGCACTAG 327
Db 320 TGGGAATTCCAAAGTATGGCACTAG 346

RESULT 3

US-10-242-535A-35025
; Sequence 35025, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005

; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35025
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-35025

Query Match 100.0%; Score 327; DB 7; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.8e-173; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 0;
QY 1 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 24 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 83
QY 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATGTGGTTGAT 120
Db 84 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATGTGGTTGAT 143
QY 121 AACTGTGCCATCTGCAGGAACCACTATTATGGATCTTTTGCATAGAAATGCTCAAGCTAACCCAG 180
Db 144 AACTGTGCCATCTGCAGGAACCACTATTATGGATCTTTTGCATAGAAATGCTCAAGCTAACCCAG 203
QY 181 GCGTCCGCTACTTTCAGAAAGTGTACTGTGCGATGGGGAGTCTGTAAACCATGCTTTTTCAC 240
Db 204 GCGTCCGCTACTTTCAGAAAGTGTACTGTGCGATGGGGAGTCTGTAAACCATGCTTTTTCAC 263
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAACAGAG 300
Db 264 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAACAGAG 323
QY 301 TGGGAATTCCAAAGTATGGCACTAG 327
Db 324 TGGGAATTCCAAAGTATGGCACTAG 350

RESULT 4

US-10-085-783A-35025
; Sequence 35025, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35025
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-35025

Query Match 100.0%; Score 327; DB 7; Length 453;


```
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46292
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-46292

Query Match      100.0%; Score 327; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.8e-173;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGCGATGGATGCGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 19 ATGGCGCAGCGATGGATGCGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 78
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 79 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 138
QY 121 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTTGCATAGAAATGTCAAGCTAACCCAG 180
Db 139 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTTGCATAGAAATGTCAAGCTAACCCAG 198
QY 181 GCGTCGCGTACTTCAGAAAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 199 GCGTCGCGTACTTCAGAAAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTTCAC 258
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 300
Db 259 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 318
QY 301 TGGGAATTCCAAAGTATGGGCACTAG 327
Db 319 TGGGAATTCCAAAGTATGGGCACTAG 345

RESULT 14
US-09-918-995-17191
; Sequence 17191, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17191
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-17191

Query Match      99.4%; Score 325; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.4e-172;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGCGCAGCGATGGATGCGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAGCG 62
Db 74 GCGCGCAGCGATGGATGCGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAGCG 133
QY 63 CTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 122
Db 134 CTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 193
QY 123 CTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTTGCATAGAAATGTCAAGCTAACCCAGGC 182
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; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46292
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-46292

Query Match      100.0%; Score 327; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.8e-173;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGCGATGGATGCGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 19 ATGGCGCAGCGATGGATGCGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 78
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 79 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 138
QY 121 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTTGCATAGAAATGTCAAGCTAACCCAG 180
Db 139 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTTGCATAGAAATGTCAAGCTAACCCAG 198
QY 181 GCGTCGCGTACTTCAGAAAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 199 GCGTCGCGTACTTCAGAAAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTTCAC 258
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 300
Db 259 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 318
QY 301 TGGGAATTCCAAAGTATGGGCACTAG 327
Db 319 TGGGAATTCCAAAGTATGGGCACTAG 345

RESULT 13
US-10-085-783A-46292
; Sequence 46292, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46292
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Db 194 CTGTGCCATCTGCAGGAACACATTATGGATCTTTGCATAGAATGTCAAGCTAACCCAGGC 253
QY 183 GTCGGCTACTTTCAGAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTTTCACTT 242
Db 254 GTCGGCTACTTTCAGAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTTTCACTT 313
QY 243 CCATCGATCTCTCGTGGCTCAAAACACACAGGAGTGTGCCATTGGACAACAGAGAGTG 302
Db 314 CCATCGATCTCTCGTGGCTCAAAACACACAGGAGTGTGCCATTGGACAACAGAGAGTG 373
QY 303 GGAATTCAAAAGTATGGCACTAG 327
Db 374 GGAATTCAAAAGTATGGCACTAG 398

RESULT 15

US-10-198-846-11311/c
; Sequence 11311, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11311
; LENGTH: 4543
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-11311

Query Match 98.2%; Score 321; DB 5; Length 4543;
Best Local Similarity 100.0%; Pred. No. 4.3e-170;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 66
Db 1085 GCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 1026
QY 67 GAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGATAACTGT 126
Db 1025 GAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGATAACTGT 966
QY 127 GCATCTGCAGGAACACACATTATGGATCTTTTGCATAGATGTCAAGCTAACAGGCGTCC 186
Db 965 GCATCTGCAGGAACACACATTATGGATCTTTTGCATAGATGTCAAGCTAACAGGCGTCC 906
QY 187 GCTACTTCAGAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTTTCACCTCCAC 246
Db 905 GCTACTTCAGAGAGTGTACTGTCGCATGGGAGTCTGTAAACCATGCTTTTTCACCTCCAC 846
QY 247 TGCATCTCTCGTGGCTCAAAACACACAGGAGTGTGTCCATTGGACAACAGAGTGGGAA 306
Db 845 TGCATCTCTCGTGGCTCAAAACACACAGGAGTGTGTCCATTGGACAACAGAGTGGGAA 786
QY 307 TTCCAAAAGTATGGCACTAG 327
Db 785 TTCCAAAAGTATGGCACTAG 765

Search completed: March 8, 2006, 16:07:15
Job time : 538.691 secs

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(without alignments)
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Perfect score: 327
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 12

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	482	3	US-09-513-999C-3894
2	327	100.0	507	3	US-09-949-016-4940
3	327	100.0	508	3	US-09-914-324A-3
4	249	76.1	3208	3	US-09-780-016-27
5	249	76.1	3208	3	US-10-214-811-27
6	249	76.1	3208	3	US-10-766-074-27
7	170	52.0	402	3	US-09-513-999C-10371
8	170	52.0	433	3	US-09-621-376-15180
9	89	27.2	25274	3	US-09-949-016-16682
10	50	15.3	504	3	US-09-914-324A-5
11	36	11.0	601	3	US-09-949-016-174803
12	20	6.1	411	3	US-09-640-211A-1731
13	18	5.5	287	3	US-09-270-767-26361
14	18	5.5	902	3	US-09-270-767-10881
15	18	5.5	3183	2	US-08-939-218A-1
16	18	5.5	3187	6	PCT-US95-068115-1
17	18	5.5	3192	2	US-08-706-037-26
18	18	5.5	3192	2	US-08-940-661A-1
19	18	5.5	3192	2	US-09-083-485-1
20	18	5.5	3192	2	US-09-005-397-26
21	18	5.5	4118	2	US-08-119-125A-3
22	18	5.5	63563	3	US-09-596-002-33
23	18	5.5	113283	3	US-09-949-016-16976
24	18	5.5	113283	3	US-09-949-016-16977

25	18	5.5	119649	3	US-09-949-016-12537	Sequence 12537, A
26	17	5.2	444	3	US-09-533-559-2439	Sequence 2439, Ap
27	17	5.2	601	3	US-09-949-016-79297	Sequence 79297, A
c 28	17	5.2	601	3	US-09-949-016-174631	Sequence 174631, A
29	17	5.2	1722	3	US-09-142-623-14	Sequence 14, Appl
30	17	5.2	1839	3	US-09-508-264A-4	Sequence 4, Appl
31	17	5.2	1894	3	US-09-508-264A-13	Sequence 13, Appl
32	17	5.2	2396	3	US-09-221-017B-74	Sequence 74, Appl
33	17	5.2	2983	3	US-09-058-489-86	Sequence 86, Appl
c 34	17	5.2	5913	3	US-09-949-016-16395	Sequence 16395, A
c 35	17	5.2	6452	3	US-09-949-016-1597	Sequence 597, App
c 36	17	5.2	6453	3	US-09-949-016-1533	Sequence 1533, Ap
c 37	17	5.2	9439	3	US-09-058-489-89	Sequence 89, Appl
c 38	17	5.2	38566	3	US-09-949-016-15271	Sequence 15271, A
c 39	17	5.2	38566	3	US-09-949-016-15272	Sequence 15272, A
c 40	17	5.2	46794	3	US-09-949-016-12399	Sequence 12399, A
c 41	17	5.2	74527	3	US-09-949-016-12339	Sequence 12339, A
c 42	17	5.2	74528	3	US-09-949-016-13275	Sequence 13275, A
c 43	17	5.2	84525	3	US-09-949-016-16678	Sequence 16678, A
c 44	17	5.2	229354	3	US-09-705-400-64	Sequence 64, Appl
c 45	17	5.2	784019	3	US-09-949-016-14033	Sequence 14033, A

ALIGNMENTS

RESULT 1
US-09-513-999C-3894
; Sequence 3894, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3894
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29..352
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 404
; OTHER INFORMATION: m=a or c
US-09-513-999C-3894

Query Match 100.0%; Score 327; DB 3; Length 482;
Best Local Similarity 100.0%; Pred No. 7.3e-167;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCGCGCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db	29	ATGCGCGCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 88
QY	61	CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db	89	CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 148
QY	121	AACTGTGCCATCTGCAGGAACCACTTATGATGCTTTTGCATAGATGCTCAAGCTAACCAAG 180

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149  AACGTGCCATCTGCAGAACCACTATTGGATCTTTGCATAGAAATGTCAGGCTAACGAG 208
181  GCGTCCGCTACTTTCAGAAAGAGTGTACTGTCGCATGGGGAGTCTGTAAACCATGCTTTTCAC 240
209  GCGTCCGCTACTTTCAGAAAGAGTGTACTGTCGCATGGGGAGTCTGTAAACCATGCTTTTCAC 268
241  TTCACATGCAATCTTCGCTGGCTCAAAACACGACAGGAGTGTGCCATTGGACAACACAGAGAG 300
269  TTCACATGCAATCTTCGCTGGCTCAAAACACGACAGGAGTGTGCCATTGGACAACACAGAGAG 328
301  TGGGAATTCCAAAGATATGGGCACCTAG 327
329  TGGGAATTCCAAAGATATGGGCACCTAG 355

RESULT 2
US-09-949-016-4940
; Sequence 4940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE
; METHODS OF DETECTION AND USES THEREOF
```

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; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-780-016-27

Query Match          76.1%; Score 249; DB 3; Length 3208;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 249; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTGGCACTCTGCAGG 138
DB 2776 TGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTGGCACTCTGCAGG 2835

QY 139 AACCACATTATGGATCTTTTGCATAGAAATGTCAAGCTAACACAGGCGTCCGCTACTTCAGAA 198
DB 2836 AACCACATTATGGATCTTTTGCATAGAAATGTCAAGCTAACACAGGCGTCCGCTACTTCAGAA 2895

QY 199 GAGTGTACTGTCCGATGGGAGTCTGTAAACATGCTTTTCACTTCCACTGCATCTCTCGC 258
DB 2896 GAGTGTACTGTCCGATGGGAGTCTGTAAACATGCTTTTCACTTCCACTGCATCTCTCGC 2955

QY 259 TGGCTCAAAACACAGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT 318
DB 2956 TGGCTCAAAACACAGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT 3015

QY 319 GGGCACTAG 327
DB 3016 GGGCACTAG 3024

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RESULT 5
US-10-214-811-27
; Sequence 27, Application US/10214811
; Patent No. 6743621
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6743621el Human Proteases and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/214,811
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-214-811-27

Query Match          76.1%; Score 249; DB 3; Length 3208;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 249; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTGGCACTCTGCAGG 138
DB 2776 TGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTGGCACTCTGCAGG 2835

QY 139 AACCACATTATGGATCTTTTGCATAGAAATGTCAAGCTAACACAGGCGTCCGCTACTTCAGAA 198
DB 2836 AACCACATTATGGATCTTTTGCATAGAAATGTCAAGCTAACACAGGCGTCCGCTACTTCAGAA 2895

QY 199 GAGTGTACTGTCCGATGGGAGTCTGTAAACATGCTTTTCACTTCCACTGCATCTCTCGC 258
DB 2896 GAGTGTACTGTCCGATGGGAGTCTGTAAACATGCTTTTCACTTCCACTGCATCTCTCGC 2955

QY 259 TGGCTCAAAACACAGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT 318
DB 2956 TGGCTCAAAACACAGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT 3015

QY 319 GGGCACTAG 327
DB 3016 GGGCACTAG 3024

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; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-780-016-27

Query Match          76.1%; Score 249; DB 3; Length 3208;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 249; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTGGCACTCTGCAGG 138
DB 2776 TGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTGGCACTCTGCAGG 2835

QY 139 AACCACATTATGGATCTTTTGCATAGAAATGTCAAGCTAACACAGGCGTCCGCTACTTCAGAA 198
DB 2836 AACCACATTATGGATCTTTTGCATAGAAATGTCAAGCTAACACAGGCGTCCGCTACTTCAGAA 2895

QY 199 GAGTGTACTGTCCGATGGGAGTCTGTAAACATGCTTTTCACTTCCACTGCATCTCTCGC 258
DB 2896 GAGTGTACTGTCCGATGGGAGTCTGTAAACATGCTTTTCACTTCCACTGCATCTCTCGC 2955

QY 259 TGGCTCAAAACACAGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT 318
DB 2956 TGGCTCAAAACACAGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT 3015

QY 319 GGGCACTAG 327
DB 3016 GGGCACTAG 3024

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RESULT 6
US-10-766-074-27
; Sequence 27, Application US/10766074
; Patent No. 6881563
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6881563el Human Proteases and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/766,074
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/10/214,811
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-074-27

Query Match          76.1%; Score 249; DB 3; Length 3208;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 249; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTGGCACTCTGCAGG 138
DB 2776 TGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATTAAGTGGCACTCTGCAGG 2835

QY 139 AACCACATTATGGATCTTTTGCATAGAAATGTCAAGCTAACACAGGCGTCCGCTACTTCAGAA 198
DB 2836 AACCACATTATGGATCTTTTGCATAGAAATGTCAAGCTAACACAGGCGTCCGCTACTTCAGAA 2895

QY 199 GAGTGTACTGTCCGATGGGAGTCTGTAAACATGCTTTTCACTTCCACTGCATCTCTCGC 258
DB 2896 GAGTGTACTGTCCGATGGGAGTCTGTAAACATGCTTTTCACTTCCACTGCATCTCTCGC 2955

QY 259 TGGCTCAAAACACAGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT 318
DB 2956 TGGCTCAAAACACAGACAGAGTGTGCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTAT 3015

QY 319 GGGCACTAG 327
DB 3016 GGGCACTAG 3024

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RESULT 7

; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(344)
; OTHER INFORMATION: Rbx1
US-09-914-324A-5

Query Match 15.3%; Score 50; DB 3; Length 504;
Best Local Similarity 100.0%; Pred. No. 6.1e-17;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 ATTGTGGTGTGTAACCTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTG 158
Db 126 ATTGTGGTGTGTAACCTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTG 175

RESULT 11
US-09-949-016-174803
; Sequence 174803, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174803
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-174803

Query Match 11.0%; Score 36; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 158 GCATAGATGTCAAGCTAACGAGCGTCCGCTACTT 193
Db 566 GCATAGATGTCAAGCTAACGAGCGTCCGCTACTT 601

RESULT 12
US-09-640-211A-1731
; Sequence 1731, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1731
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Pinus radiata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(411)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-211A-1731

Query Match 6.1%; Score 20; DB 3; Length 411;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 TGGGATATTGTGGTTGATAA 122
Db 206 TGGGATATTGTGGTTGATAA 225

RESULT 13
US-09-270-767-26361/c
; Sequence 26361, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26361
; LENGTH: 287
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-26361

Query Match 5.5%; Score 18; DB 3; Length 287;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 AGTGGGAATTCCAAAGT 316
Db 113 AGTGGGAATTCCAAAGT 96

RESULT 14
US-09-270-767-10881/c
; Sequence 10881, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10881
; LENGTH: 902
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-10881

Query Match 5.5%; Score 18; DB 3; Length 902;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 AGTGGGAATTCCAAAGT 316

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Db      |||||||
       728 AGTGGGAATTCCAAAAGT 711

RESULT 15
US-08-939-218A-1/c
; Sequence 1, Application US/08939218A
; Patent No. 5981243
; GENERAL INFORMATION:
; APPLICANT: BERKA, Randy Michael
; APPLICANT: BROWN, Stephen H.
; APPLICANT: XU, Feng
; APPLICANT: SCHNEIDER, Palle
; APPLICANT: OXENB LL, Karen M.
; APPLICANT: AASLYNG, Dorrit A.
; TITLE OF INVENTION: PURIFIED MYCELIOPTHORA LACCASES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5981243o No. 5981243disk of No. 5981243th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,218A
; FILING DATE: 29-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol E.
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 4184.120-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; LENGTH: 3183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(586..831, 917..994, 1079..1090, 1193..1264,
; LOCATION: 1337..2308, 2456..2524, 2618..3028)
US-08-939-218A-1

Query Match      5.5%; Score 18; DB 2; Length 3183;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      198 AGAGTGACTGTGCGCATG 215
Db      |||||||
       924 AGAGTGACTGTGCGCATG 907

Search completed: March 8, 2006, 14:34:35
Job time : 114.91 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 10:15:10 ; Search time 3736 Seconds

(without alignments)

4095.122 Million cell updates/sec

Title: US-09-541-462B-1

Perfect score: 327

Sequence: 1 atggcgcagcgtgatgt.....tccaaagatgggactag 327

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size: 12

Total number of hits satisfying chosen parameters: 897482

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

EST:*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*
- 10: gb_est10.*
- 11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	327	100.0	462	7	CN305890 170005830
2	327	100.0	471	2	BG339057 602436882
3	327	100.0	473	5	BX283972 BX283972
4	327	100.0	488	6	BG777485 602664820
5	327	100.0	498	6	CB296618 12822006
6	327	100.0	509	7	CN305892 170006001
7	327	100.0	518	3	BP420485 BP420485
8	327	100.0	522	1	AL711573 DKFZp6861
9	327	100.0	525	2	BG337472 602435003
10	327	100.0	527	3	BW715215 UI-E-CL1-
11	327	100.0	527	5	BW715215 UI-E-CL1-
12	327	100.0	527	6	CB999822 AGENCOURT
13	327	100.0	529	3	BW757406 K-EST0036
14	327	100.0	531	6	CD523457 AGENCOURT
15	327	100.0	533	5	BW729963 UI-E-CK1-
16	327	100.0	537	2	BG478622 602525509
17	327	100.0	545	5	BW941262 AGENCOURT
18	327	100.0	546	2	B1198015 602762132
19	327	100.0	546	5	BW601181 AGENCOURT
20	327	100.0	548	1	AV716338 AV716338
21	327	100.0	548	5	BW601301 AGENCOURT
22	327	100.0	549	3	B1858425 603386437

23	327	100.0	550	5	BU955646
24	327	100.0	554	6	CD249363
25	327	100.0	555	5	BU532840
26	327	100.0	555	5	BU601080
27	327	100.0	557	5	BU954591
28	327	100.0	558	6	CD388268
29	327	100.0	559	7	CK003869
30	327	100.0	562	6	CD175085
31	327	100.0	563	5	BU861191
32	327	100.0	570	5	BU597842
33	327	100.0	573	5	BU533405
34	327	100.0	581	3	BP308845
35	327	100.0	583	3	BP317451
36	327	100.0	616	2	BG705958
37	327	100.0	736	2	BG503311
38	327	100.0	801	5	BU533420
39	327	100.0	845	5	BU959349
40	327	100.0	886	2	BG481544
41	327	100.0	904	3	BM459634
42	327	100.0	945	3	BQ216738
43	327	100.0	1098	3	BQ050461
44	326	99.7	403	2	BG531117
45	326	99.7	448	2	BE738587

ALIGNMENTS

RESULT 1
CN305890 170005830 462 bp mRNA linear EST 16-MAY-2004
LOCUS GRN_PRESHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN305890
VERSION CN305890.1 GI:47322304
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (Bases 1 to 462)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Gen Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@gen.com
Insert Length: 462 Std Error: 0.00.
FEATURES
Location/Qualifiers
source
1..462
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PRESHEP"
/notes="oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN

Query Match 100.0%; Score 327; DB 7; Length 462;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
23 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 82
Qy 61 CGCTTTGAAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
83 CGCTTTGAAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 142
Qy 121 AACTGTGCCATCTGCAGGAACCAACATATGATGATCTTTGCATAGATGCTCAAGCTAACAG 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
143 AACTGTGCCATCTGCAGGAACCAACATATGATGATCTTTGCATAGATGCTCAAGCTAACAG 202
Qy 181 GCGTCCGCTACTTCAGAGAGTGACTGTGCGATGGGAGTCTGTACCACTGCTTTTTCAC 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
203 GCGTCCGCTACTTCAGAGAGTGACTGTGCGATGGGAGTCTGTACCACTGCTTTTTCAC 262
Qy 241 TTCCACTGTCATCTCTCGCTGGCTCAAAACACAGCAGGTGTCTCATTTGGACAAACAGAG 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
263 TTCCACTGTCATCTCTCGCTGGCTCAAAACACAGCAGGTGTCTCATTTGGACAAACAGAG 322
Qy 301 TGGGAATTCACAAAGTATGGCACTAG 327
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
323 TGGGAATTCACAAAGTATGGCACTAG 349

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RESULT 2
BG339057 602436882F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4554597 5',
LOCUS mRNA sequence.
DEFINITION BG339057.1 GI:13145495
VERSION EST.
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 471)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-roman.nhl.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1254 row: d column: 22
High quality sequence stop: 470.
Location/Qualifiers
1. .471
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4554597"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"

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FEATURES
source
1. .471
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4554597"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

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ORIGIN

```

Query Match 100.0%; Score 327; DB 2; Length 471;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
42 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 101
Qy 61 CGCTTTGAAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
102 CGCTTTGAAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 161
Qy 121 AACTGTGCCATCTGCAGGAACCAACATATGATGATCTTTGCATAGATGCTCAAGCTAACAG 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
162 AACTGTGCCATCTGCAGGAACCAACATATGATGATCTTTGCATAGATGCTCAAGCTAACAG 221
Qy 181 GCGTCCGCTACTTCAGAGAGTGACTGTGCGATGGGAGTCTGTACCACTGCTTTTTCAC 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
222 GCGTCCGCTACTTCAGAGAGTGACTGTGCGATGGGAGTCTGTACCACTGCTTTTTCAC 281
Qy 241 TTCCACTGTCATCTCTCGCTGGCTCAAAACACAGCAGGTGTCTCATTTGGACAAACAGAG 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
282 TTCCACTGTCATCTCTCGCTGGCTCAAAACACAGCAGGTGTCTCATTTGGACAAACAGAG 341
Qy 301 TGGGAATTCACAAAGTATGGCACTAG 327
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
342 TGGGAATTCACAAAGTATGGCACTAG 368

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RESULT 3
BX283972 473 bp mRNA linear EST 05-MAR-2003
LOCUS BX283972 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:958P131435 ;
DEFINITION IMAGE:4652028, mRNA sequence.
ACCESSION BX283972
VERSION BX283972.1 GI:28848426
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 473)
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp958P131435.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
pCMV-M13u, Primer sequence: CGTTGTAACACGACGCCAGT.
Location/Qualifiers
1. .473
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp958P131435 ; IMAGE:4652028"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;

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FEATURES

source

1. .473

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGp958P131435 ; IMAGE:4652028"

/tissue_type="choriocarcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_21"

/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 473;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGCGCAGCGATGGATGGATACCCCGCGCGCACCAACAGCGCGCGGCAAGAAG 60
 Db ATGCGCGCAGCGATGGATGGATACCCCGCGCGCACCAACAGCGCGCGGCAAGAAG 66

Qy 61 CGCTTTGAAGTGAAAGAGTGAATGCAATGATGATCTTTGCGCTGGGATATTGTTGAT 120
 Db CGCTTTGAAGTGAAAGAGTGAATGCAATGATGATCTTTGCGCTGGGATATTGTTGAT 126

Qy 121 AACTGTGCTACTCTGCGAGAACCAATATGATCTTTGATAGATGTCAGCTTAACAG 180
 Db 127 AACTGTGCTACTCTGCGAGAACCAATATGATCTTTGATAGATGTCAGCTTAACAG 186

Qy 181 GCGTCCGCTACTCTCAGAGAGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTAC 240
 Db 187 GCGTCCGCTACTCTCAGAGAGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTAC 246

Qy 241 TTCACATGCTACTCTGCTGCTCAAAACAGCAGGCTGTCCATGGACAACAGAGAG 300
 Db 247 TTCACATGCTACTCTGCTGCTCAAAACAGCAGGCTGTCCATGGACAACAGAGAG 306

Qy 301 TGGGAATTCAAAAGTAGTGGCACTAG 327
 Db 307 TGGGAATTCAAAAGTAGTGGCACTAG 333

RESULT 4
 BG777485 488 bp mRNA linear EST 15-MAY-2001
 LOCUS 60264820F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4804661 5'

mRNA sequence.

BG777485

BG777485.1 GI:14047802

EST.

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 488)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe-remail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: CLONETECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L10M1651 row: h column: 06

High quality sequence stop: 487.

Location/Qualifiers

1. 488

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4804661"

/tissue_type="adenocarcinoma"

FEATURES

source

/lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_60"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgctcgcc); Site 2: SfiI
 (ggcattatggcc); Double-stranded cDNA was prepared from
 cell line RNA. 5' and 3' adaptors were used in cloning as
 follows: 5' adaptor sequence: 5'-CAGGCCATTATGCCC-3' and
 3' adaptor sequence:
 5'-ATTCTAGAGCGGCGGCGGCACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.5
 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 327; DB 2; Length 488;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGCGCAGCGATGGATGGATACCCCGCGCGCACCAACAGCGCGGCAAGAAG 60
 Db 23 ATGCGCGCAGCGATGGATGGATACCCCGCGCGCACCAACAGCGCGGCAAGAAG 82

Qy 61 CGCTTTGAAGTGAAAGAGTGAATGCAATGATGATCTTTGCGCTGGGATATTGTTGAT 120
 Db 83 CGCTTTGAAGTGAAAGAGTGAATGCAATGATGATCTTTGCGCTGGGATATTGTTGAT 142

Qy 121 AACTGTGCTACTCTGCGAGAACCAATATGATCTTTGATAGATGTCAGCTTAACAG 180
 Db 143 AACTGTGCTACTCTGCGAGAACCAATATGATCTTTGATAGATGTCAGCTTAACAG 202

Qy 181 GCGTCCGCTACTCTCAGAGAGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTAC 240
 Db 203 GCGTCCGCTACTCTCAGAGAGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTAC 262

Qy 241 TTCACATGCTACTCTGCTGCTCAAAACAGCAGGCTGTCCATGGACAACAGAGAG 300
 Db 263 TTCACATGCTACTCTGCTGCTCAAAACAGCAGGCTGTCCATGGACAACAGAGAG 322

Qy 301 TGGGAATTCAAAAGTAGTGGCACTAG 327
 Db 323 TGGGAATTCAAAAGTAGTGGCACTAG 349

RESULT 5

CB296618

LOCUS

DEFINITION

12B22006 rev.1 C10_r_082.ab1 Chimpanzee brain library Koo's Pan
 troglodytes cDNA clone 12B22006_rev.1_C10_r_082.ab1 5', mRNA
 sequence.

CB296618

CB296618.1 GI:28622048

EST.

KEYWORDS

SOURCE

ORGANISM

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Pan.

1 (bases 1 to 498)

Heilmann, I., Zollner, S., Enard, W., Ebersberger, I., Nickel, B. and

Paabo, S.

Selection on human genes as revealed by comparisons to chimpanzee

cDNA

Genome Res. (2003) In press

Contact: Paabo S

Evolutionary Genetics

Max-Planck-Institute for evolutionary Anthropology

Deutscher Platz 6 04103 Leipzig, Germany

Tel: +49-(0)-341-3550 500

Fax: +49-(0)-341-3550 555

Email: paabo@eva.mpg.de

Seq primer: M13 reverse.

FEATURES	Location/Qualifiers	
	source	
1. .498		
/organism="Pan troglodytes"		
/mol_type="mRNA"		
/db_xref="taxon:9598"		
/clone="12B22006_rev_1_C10_r_082.ab1"		
/sex="male"		
/tissue_type="brain, presumably cortex"		
/dev_stage="adult"		
/lab_host="Epilcurian Coli (TM) XL-10-Gold"		
/clone_lib="Chimpanzee brain library Koo"		
/note="Vector: pUCHi; Site 1: Sfil-A; Site 2: Sfil-B; The library was prepared using the SMART cDNA library construction kit (Clontech), doing only primer extension, but not PCR amplification of the cDNA. The only deviation from the published protocol was that we cloned the cDNA into a plasmid Vector."		
ORIGIN		
Query Match 100.0%; Score 327; DB 6; Length 498;		
Best Local Similarity 100.0%; Pred. No. 6.6e-175;		
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	ATGGCGCAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCACAG 60
Db	2	ATGGCGCAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCACAG 61
Qy	61	CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db	62	CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 121
Qy	121	AACGTGCCATCTGCAGGAACCAATATGGATCTTTGCATAGAAATGCTCAAGCTAAC 180
Db	122	AACGTGCCATCTGCAGGAACCAATATGGATCTTTGCATAGAAATGCTCAAGCTAAC 181
Qy	181	GCCTCCGCTACTTCAGAAAGTGTACTGTGCATGGGGAGTCTGTAAACCATGCTTTT 240
Db	182	GCCTCCGCTACTTCAGAAAGTGTACTGTGCATGGGGAGTCTGTAAACCATGCTTTT 241
Qy	241	TTCCACTGCATCTCTCGCTGCCTCAAAACACAGCAGGTGTCCATTGGACACAGAG 300
Db	242	TTCCACTGCATCTCTCGCTGCCTCAAAACACAGCAGGTGTCCATTGGACACAGAG 301
Qy	301	TGGGAATTCAAAAGTATGGCACTAG 327
Db	302	TGGGAATTCAAAAGTATGGCACTAG 328
RESULT 6		
CN305892 509 bp mRNA linear EST 16-MAY-2004		
LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
Homo sapiens (human)		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
Hominidae; Homo.		
1 (bases 1 to 509)		
Bradenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,		
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,		
Lebkowski, J. and Stanton, L. W.		
Transcriptome characterization elucidates signaling networks that		
control human ES cell growth and differentiation		
Nat. Biotechnol. 22 (6), 707-716 (2004)		
15146197		
Contact: Bradenberger R		
Regenerative Medicine		
Geron Corporation		
230 Constitution Drive, Menlo Park, CA 94025, USA		
Tel: 650 473 8658		
FEATURES		
source		
1. .518		
/organism="Homo sapiens"		
/db_xref="taxon:9606"		
/tissue_type="embryonic stem cell, retinoic acid and		
mitogen-treated hES cell line H7"		
/clone_lib="GRN PRENEU"		
/note="oligo dT primed, full-length enriched cDNA library		
from hES cell line H7 (p29) maintained in feeder-free		
conditions. Embryoid bodies were generated in the presence		
of all-trans retinoic acid and mitogens."		
ORIGIN		
Query Match 100.0%; Score 327; DB 7; Length 509;		
Best Local Similarity 100.0%; Pred. No. 6.6e-175;		
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	ATGGCGCAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCACAG 60
Db	6	ATGGCGCAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCACAG 65
Qy	61	CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db	66	CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 125
Qy	121	AACGTGCCATCTGCAGGAACCAATATGGATCTTTGCATAGAAATGCTCAAGCTAAC 180
Db	126	AACGTGCCATCTGCAGGAACCAATATGGATCTTTGCATAGAAATGCTCAAGCTAAC 185
Qy	181	GCCTCCGCTACTTCAGAAAGTGTACTGTGCATGGGGAGTCTGTAAACCATGCTTTT 240
Db	186	GCCTCCGCTACTTCAGAAAGTGTACTGTGCATGGGGAGTCTGTAAACCATGCTTTT 245
Qy	241	TTCCACTGCATCTCTCGCTGCCTCAAAACACAGCAGGTGTCCATTGGACACAGAG 300
Db	246	TTCCACTGCATCTCTCGCTGCCTCAAAACACAGCAGGTGTCCATTGGACACAGAG 305
Qy	301	TGGGAATTCAAAAGTATGGCACTAG 327
Db	306	TGGGAATTCAAAAGTATGGCACTAG 332
RESULT 7		
BP420485 518 bp mRNA linear EST 27-MAY-2005		
LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
Hominidae; Homo.		
1 (bases 1 to 518)		
Takeda, J., Jin, L. and Horikawa, Y.		
Expression profile of mRNAs from human pancreatic islet tumors		
Unpublished (2005)		
Contact: Yukio Horikawa		
Laboratory of Molecular Genetics		
Institute for Molecular and Cellular Regulation, Gunma University		
Shima-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan		
Tel: 81-27-220-8832		
Fax: 81-27-220-8889		
Email: yhorikawa@showa.gunma-u.ac.jp.		
Location/Qualifiers		
1. .518		
/organism="Homo sapiens"		

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HIE03775r"
/tissue_type="small intestine"
/clone_lib="Homo sapiens small intestine"

ORIGIN

Query Match 100.0%; Score 327; DB 3; Length 518;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGGATGGATGGATACCCGAGCGGACCAACAGCGGCGGCGGCAAGAG 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 14 ATGGCGGAGGATGGATGGATACCCGAGCGGACCAACAGCGGCGGCGGCAAGAG 73
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 CGCTTTGAAGTGAAAGAGTGAATGCAGTAGCCCTCTGGGCTTGGGATATTGTGTTGAT 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 74 CGCTTTGAAGTGAAAGAGTGAATGCAGTAGCCCTCTGGGCTTGGGATATTGTGTTGAT 133
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 AACTGTGCGCATCTGCAGGAACACATTTATGATCTTTGCATAGAAATGTCAAGCTAACAG 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 134 AACTGTGCGCATCTGCAGGAACACATTTATGATCTTTGCATAGAAATGTCAAGCTAACAG 193
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACATGCTTTTCAC 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 194 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACATGCTTTTCAC 253
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 TTCACATGTCATCTCTCGCTGGCTCAAAACACAGAGGTGTGTCATTGGACACAGAGAG 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 254 TTCACATGTCATCTCTCGCTGGCTCAAAACACAGAGGTGTGTCATTGGACACAGAGAG 313
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 TGGGAATTCCTCAAAAGTATGGGCACCTAG 327
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 314 TGGGAATTCCTCAAAAGTATGGGCACCTAG 340
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 8

AL711573 522 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686i0483 r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFZp686i0483 5', mRNA sequence.

ACCESSION AL711573
VERSION AL711573.1 GI:19694928
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 522)
Koehler, K., Beyer, A., Mewes, W., Weil, B. and Wiemann, S.
EST (Koehler, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
Contact: MIPS
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert.
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.

No sl sequence available.
This clone (DKFZp686i0483) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers
1..522
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686i0483"
/dev_stage="adult"

/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplex2; Site_1: SfIIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 100.0%; Score 327; DB 1; Length 522;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGGATGGATGGATACCCGAGCGGACCAACAGCGGCGGCGGCAAGAG 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 21 ATGGCGGAGGATGGATGGATACCCGAGCGGACCAACAGCGGCGGCGGCAAGAG 80
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 CGCTTTGAAGTGAAAGAGTGAATGCAGTAGCCCTCTGGGCTTGGGATATTGTGTTGAT 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 81 CGCTTTGAAGTGAAAGAGTGAATGCAGTAGCCCTCTGGGCTTGGGATATTGTGTTGAT 140
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 AACTGTGCGCATCTGCAGGAACACATTTATGATCTTTGCATAGAAATGTCAAGCTAACAG 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 141 AACTGTGCGCATCTGCAGGAACACATTTATGATCTTTGCATAGAAATGTCAAGCTAACAG 200
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACATGCTTTTCAC 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 201 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACATGCTTTTCAC 260
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 TTCACATGTCATCTCTCGCTGGCTCAAAACACAGAGGTGTGTCATTGGACACAGAGAG 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 261 TTCACATGTCATCTCTCGCTGGCTCAAAACACAGAGGTGTGTCATTGGACACAGAGAG 320
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 TGGGAATTCCTCAAAAGTATGGGCACCTAG 327
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 321 TGGGAATTCCTCAAAAGTATGGGCACCTAG 347
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 9

BG337472 525 bp mRNA linear EST 27-FEB-2001
LOCUS 602435003F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4553064 5',
DEFINITION mRNA sequence.

ACCESSION BG337472
VERSION BG337472.1 GI:13143910
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 525)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI250 row: e column: 01

High quality sequence stop: 525.

Location/Qualifiers

FEATURES

source
1..525
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4553064"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:

Email: cgapbs-remail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2955 row: e column: 17
 High quality sequence stop: 498.

FEATURES

source

1. 527
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6673337"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_127"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggcgctcgcc); Double-stranded cDNA was
 prepared from a pool of 40 cell line polyA+ RNAs (bladder
 - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
 kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
 salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
 adaptors were used in cloning as follows:
 5'-AAGCAGTGTATCAGCAGATGGCCATAGCGCCGG-3' and
 5'-ATTCTAGGCGGAGCGCGGCATG-dt(30)NN-3'. Full-length
 enriched library was constructed using the Clontech
 Creator SMART kit and size-selected to contain the 1-2 kb
 size fraction (other fractions present in NIH_MGC 126 and
 NIH_MGC 128). Library created in the laboratory of T.
 Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 527;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGGGCAAGAAG 60
 Db 24 ATGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGGGCAAGAAG 83

Qy 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTTGGTTGAT 120
 Db 84 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTTGGTTGAT 143

Qy 121 AACTGTGCCATCTCGAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTAACCG 180
 Db 144 AACTGTGCCATCTCGAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTAACCG 203

Qy 181 CGCTCCGCTACTCTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
 Db 204 CGCTCCGCTACTCTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 263

Qy 241 TTCCACTGTCATCTCTCGTGGCTCAAAACAGCAGCAGGTGTCTCAATGGACACAGAGAG 300
 Db 264 TTCCACTGTCATCTCTCGTGGCTCAAAACAGCAGCAGGTGTCTCAATGGACACAGAGAG 323

Qy 301 TGGGAATTCCAAAGTATGGCACTAG 327
 Db 324 TGGGAATTCCAAAGTATGGCACTAG 350

RESULT 12

CB999822 527 bp mRNA linear EST 01-MAY-2003
 LOCUS
 DEFINITION AGENCOURT 13645988 NIH_MGC_186 Homo sapiens cDNA clone
 IMAGE:30322649 5', mRNA sequence.
 CB999822
 ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CB999822.1 GI:30294342

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 527)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDCM123 row: p column: 18

High quality sequence stop: 518.

Location/Qualifiers

1. 527

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30322649"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_186"

/note="Organ: Pooled-Skin; Vector: pDNR-LIB; Site 1: SfiI

(ggccattatggcc); Site 2: SfiI (ggcgctcgcc); Library is

oligo-dt primed and directionally cloned. cDNA was

prepared from a pooled samples of tissues from Skin,

meninges, duramater, pia mater and choroid plexus.

and 3' adaptors were used in cloning as follows: 5'

sequence: 5'-ATTCTAGGCGGAGCGGCATG-dt(30)NN-3'

(where B = A, C, or G and N = A, C, G, or T). Average

insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies

contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech

Laboratories (Palo Alto, CA). Note: this is a NIH_MGC

Library"

ORIGIN

Query Match 100.0%; Score 327; DB 6; Length 527;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGGGCAAGAAG 60
 Db 25 ATGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGGGCAAGAAG 84

Qy 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTTGGTTGAT 120
 Db 85 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTTGGTTGAT 144

Qy 121 AACTGTGCCATCTCGAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTAACCG 180
 Db 145 AACTGTGCCATCTCGAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTAACCG 204

Qy 181 GCCTCCGCTACTCTCAGAAAGTGTACTGTGCGATGGGAGTCTGTACCATGCTTTTCAC 240
 Db 205 GCCTCCGCTACTCTCAGAAAGTGTACTGTGCGATGGGAGTCTGTACCATGCTTTTCAC 264

Qy 241 TTCCACTGTCATCTCTCGCTGGCTCAAAACAGCAGCAGGTGTCTCAATGGACACAGAGAG 300
 Db 265 TTCCACTGTCATCTCTCGCTGGCTCAAAACAGCAGCAGGTGTCTCAATGGACACAGAGAG 324

Qy 301 TGGGAATTCCAAAGTATGGCACTAG 327
 Db 325 TGGGAATTCCAAAGTATGGCACTAG 351


```

RESULT 13
BM757406
LOCUS
DEFINITION
    BM757406 529 bp mRNA linear EST 04-MAR-2002
    K-EST0036388 SISNU5 Homo sapiens cDNA clone S1SNUS-29-H12 5', mRNA
sequence.
ACCESSION
BM757406
VERSION
BM757406.1 GI:19087021
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 529)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
TITLE
Unpublished (2002)
JOURNAL
COMMENT
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yusong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 29 Row: H Column: 12
High quality sequence stop: 529.
FEATURES
source
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="S1SNUS-29-H12"
        /sex="F"
        /tissue_type="Ascites"
        /cell_type="Lymphoblast-like"
        /lab_host="SNU-5"
        /lab_host="Top10P"
        /clone_lib="S1SNUS"
        /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
        Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
        bacterial alkaline phosphatase (BAP) and then decapped
        with tabacco acid pyrophosphatase (TAP). The decapped
        intact mRNA was ligated with DNA-RNA linker including EcoR
        I site by treatment of T4 RNA ligase and the first strand
        cDNA was synthesized from oligo dt-selected mRNA by
        priming with dt-tailed vector. The dt-tailed vector was
        adjusted to have about 60nt. The cDNA vector was
        circularized with E. coli DNA ligase after digestion of
        EcoRI which site is also included in vector. An RNA strand
        converted to a DNA strand by Okayama-Berg method. The
        obtained cDNA vectors were used for transformation of
        competent cells E. coli Top10P by electroporation method.
        The cDNA libraries constructed by this method are
        full-length enriched cDNA library."
ORIGIN
Query Match 100.0%; Score 327; DB 3; Length 529;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGACGAGTGATGGATATACCCGAGCGGCACACACGCGGGGCAAGAAG 60
|
|
|
Db 33 ATGGCGGACGAGTGATGGATATACCCGAGCGGCACACACGCGGGGCAAGAAG 92
|
|
|
Qy 61 CGCTTTGAAGTGAAGTGAATGCAGTACCCCTCTGGGCTTGGGATATTGTGTTGAT 120
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|
|
Db 93 CGCTTTGAAGTGAAGTGAATGCAGTACCCCTCTGGGCTTGGGATATTGTGTTGAT 152
|
|
|
Qy 121 AACTGTGCCATCTCGAGGAACACATATGGAATCTTTGCATAGATGTCAAGCTAACGAG 180
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|

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Db 153 AACTGTGCCATCTCGAGGAACACATATGGAATCTTTGCATAGATGTCAAGCTAACGAG 212
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Qy 181 GGTTCGGCTACTTCAGAGAGTGTAATGTCGATGGGAGTCTGTAAACCATGCTTTTTCAC 240
|
|
|
Db 213 GGTTCGGCTACTTCAGAGAGTGTAATGTCGATGGGAGTCTGTAAACCATGCTTTTTCAC 272
|
|
|
Qy 241 TTCCACTGCATCTTCGCTGGCTCAAAACACACACAGGTGTGTCCATTGGACAAACAGAGAG 300
|
|
|
Db 273 TTCCACTGCATCTTCGCTGGCTCAAAACACACAGGTGTGTCCATTGGACAAACAGAGAG 332
|
|
|
Qy 301 TGGGAATTCCTCAAAAGTATGGCACTAG 327
|
|
|
Db 333 TGGGAATTCCTCAAAAGTATGGCACTAG 359
|
|
|
RESULT 14
CD523457
LOCUS
DEFINITION
    CD523457 531 bp mRNA linear EST 06-JUN-2003
    AGENCOURT 14360071 NIH_MGC_191 Homo sapiens cDNA clone
    IMAGE:30412182 5', mRNA sequence.
ACCESSION
CD523457
VERSION
CD523457.1 GI:31455175
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 531)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: NDCM205 row: c column: 07
High quality sequence stop: 518.
FEATURES
source
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:30412182"
        /tissue_type="Pooled"
        /lab_host="DH10B (TI phage-resistant)"
        /clone_lib="NIH_MGC_191"
        /note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
        Site_2: SfiI (ggcgcttcggcc); Library is oligo-dt primed
        and directionally cloned. PBMC - Peripheral Blood
        Mononuclear Cells. RNA was pooled from 3/6hour stimulation
        with PMA adn Ionomycin. 5' and 3' adaptors were used in
        cloning as follows: 5' adaptor sequence:
        5'-CAGGCTTATGCCC-3, and 3' adaptor sequence:
        5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A,
        C, G and N = A, C, G, or T). Average insert size 1.69
        kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
        by PCR. This library was enriched for full-length clones
        and was constructed by Clontech Laboratories (Palo Alto,
        CA). Note: this is a NIH_MGC Library."
ORIGIN
Query Match 100.0%; Score 327; DB 6; Length 531;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;

```


Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGAGGATGGATGTGGATACCCCGAGCGCACCACAGCGCGCGGCAAGAAG 60
 |||||
 Db 23 ATGGCGGAGGATGGATGTGGATACCCCGAGCGCACCACAGCGCGCGGCAAGAAG 82
 |||||

Qy 61 CGCTTTGAAGTGAAAGTGAATGAGTACCTCTGGGCTCTGGGATATTGTGGTTGAT 120
 |||||
 Db 83 CGCTTTGAAGTGAAAGTGAATGAGTACCTCTGGGCTCTGGGATATTGTGGTTGAT 142
 |||||

Qy 121 AACTGTGTCATCTGCAGAACACCATTTATGATCTTTGCATAGATGTCAGCTAACCCAG 180
 |||||
 Db 143 AACTGTGTCATCTGCAGAACACCATTTATGATCTTTGCATAGATGTCAGCTAACCCAG 202
 |||||

Qy 181 CGCTCCGCTACTCTCAGAGAGTACTGTGCGATGGGAGTCTGTAAACCATCTTTTCAC 240
 |||||
 Db 203 CGCTCCGCTACTCTCAGAGAGTACTGTGCGATGGGAGTCTGTAAACCATCTTTTCAC 262
 |||||

Qy 241 TTCACATGCTCTCTCGCTGGCTCAAAACAGACAGGTGTGTCCATTGGACAAACAGAGAG 300
 |||||
 Db 263 TTCACATGCTCTCTCGCTGGCTCAAAACAGACAGGTGTGTCCATTGGACAAACAGAGAG 322
 |||||

Qy 301 TGGGAATTCCAAAGTATGGCACTAG 327
 |||||
 Db 323 TGGGAATTCCAAAGTATGGCACTAG 349
 |||||

RESULT 15

BU729963/c

LOCUS BU729963 533 bp mRNA linear EST 09-OCT-2002

DEFINITION UI-E-CK1-afi-h-19-0-UI.s1 UI-E-CK1 Homo sapiens cDNA clone

ACCESSION BU729963

VERSION BU729963.1 GI:23653376

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 533)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene discovery

Genome Res. 6 (9), 791-806 (1996)

889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

1..533

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-E-CK1-afi-h-19-0-UI"

/tissue_type="Retina Foveal and Macular"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-E-CK1"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;

UI-E-CK1 is a normalized cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

TAG TISSUE=Foveal and Macular Retina

TAG_LIB=UI-E-CK1

TAG_SEQ=GTCC"

ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 533;
 Best Local Similarity. 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGAGGATGGATGTGGATACCCCGAGCGCACCACAGCGCGCGGCAAGAAG 60
 |||||
 Db 518 ATGGCGGAGGATGGATGTGGATACCCCGAGCGCACCACAGCGCGCGGCAAGAAG 459
 |||||

Qy 61 CGCTTTGAAGTGAAAGTGAATGAGTACCTCTGGGCTCTGGGATATTGTGGTTGAT 120
 |||||
 Db 458 CGCTTTGAAGTGAAAGTGAATGAGTACCTCTGGGCTCTGGGATATTGTGGTTGAT 399
 |||||

Qy 121 AACTGTGCCATCTGCAGAACACCATTTATGATCTTTGCATAGATGTCAGCTAACCCAG 180
 |||||
 Db 398 AACTGTGCCATCTGCAGAACACCATTTATGATCTTTGCATAGATGTCAGCTAACCCAG 339
 |||||

Qy 181 GCGTCCGCTACTCTCAGAAAGATGTACTGTGCGATGGGAGTCTGTAAACCATCTTTTCAC 240
 |||||
 Db 338 GCGTCCGCTACTCTCAGAAAGATGTACTGTGCGATGGGAGTCTGTAAACCATCTTTTCAC 279
 |||||

Qy 241 TTCACATGCTCTCTCGCTGGCTCAAAACAGACAGGTGTGTCCATTGGACAAACAGAGAG 300
 |||||
 Db 278 TTCACATGCTCTCTCGCTGGCTCAAAACAGACAGGTGTGTCCATTGGACAAACAGAGAG 219
 |||||

Qy 301 TGGGAATTCCAAAGTATGGCACTAG 327
 |||||
 Db 218 TGGGAATTCCAAAGTATGGCACTAG 192
 |||||

RESULT 16

BG478622

LOCUS BG478622 537 bp mRNA linear EST 21-MAR-2001

DEFINITION 602525509F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4643619 5', mRNA sequence.

ACCESSION BG478622

VERSION BG478622.1 GI:13410901

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 537)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: gcapbs-i@mail.nih.gov
 Tissue Procurement: ATCC/DCTB/DTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 546)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: ATCC
 DNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLC1786 row: 0 column: 07
 High quality sequence stop: 525.
 Location/Qualifiers
 1..546
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4897758"
 /tissue_type="neuroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 19"
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
 Query Match 100.0%; Score 327; DB 2; Length 546;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGGGGGAGGATGGATGGATACCCGAGCGGACCAACAGCGGGCGGGAAG 60
 Db 18 ATGGCGGAGGATGGATGGATACCCGAGCGGACCAACAGCGGGCGGGAAG 77
 Qy 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
 Db 78 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 137
 Qy 121 AACTGTGCGCATCTGCAGGAACACATTTATGGATCTTTGCATAGATGTCAAGCTAAC 180
 Db 138 AACTGTGCGCATCTGCAGGAACACATTTATGGATCTTTGCATAGATGTCAAGCTAAC 197
 Qy 181 CGGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTGTCTGTAACTTTTCAC 240
 Db 198 CGGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTGTCTGTAACTTTTCAC 257
 Qy 241 TTCCACTGCATCTCTCGCTGCTCAAAACAGCAGAGTGTCTCCATTGGACACAGAG 300
 Db 258 TTCCACTGCATCTCTCGCTGCTCAAAACAGCAGAGTGTCTCCATTGGACACAGAG 317
 Qy 301 TGGGAATTCCAAAGTATGGGCACCTAG 327
 Db 318 TGGGAATTCCAAAGTATGGGCACCTAG 344
 RESULT 19
 LOCUS BU601181 546 bp mRNA linear EST 20-SEP-2002
 DEFINITION AGENCOURT 10029786 NIH_MGC_142 Homo sapiens cDNA clone
 IMAGE:6495061 5', mRNA sequence.
 BU601181
 ACCESSION BU601181
 VERSION BU601181.1 GI:23252940
 KEYWORDS EST.

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 546)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2672 row: e column: 14
 High quality sequence stop: 491.
 Location/Qualifiers
 1..546
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6495061"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (Ti-phage-resistant)"
 /clone_lib="NIH_MGC_142"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgcctggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
 5'-AAGCAGGTATCAACGACGATGGCCATTACGGCGG-3' and
 5'-ATTCTAGAGCGGCGGCGGACATG-DT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH_MGC_141). Library created in the laboratory of M. Brownstein (NIH). Note: this is a NIH_MGC Library."
 Query Match 100.0%; Score 327; DB 5; Length 546;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGGCGGAGGATGGATGGATACCCGAGCGGACCAACAGCGGGCGGGAAG 60
 Db 13 ATGGCGGAGGATGGATGGATACCCGAGCGGACCAACAGCGGGCGGGAAG 72
 Qy 61 CGCTTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
 Db 73 CGCTTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 132
 Qy 121 AACTGTGCGCATCTGCAGGAACACATTTATGGATCTTTGCATAGATGTCAAGCTAAC 180
 Db 133 AACTGTGCGCATCTGCAGGAACACATTTATGGATCTTTGCATAGATGTCAAGCTAAC 192
 Qy 181 CGGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTGTCTGTAACTTTTCAC 240
 Db 193 CGGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTGTCTGTAACTTTTCAC 252
 Qy 241 TTCCACTGCATCTCTCGCTGCTCAAAACAGCAGAGTGTCTCCATTGGACACAGAG 300
 Db 253 TTCCACTGCATCTCTCGCTGCTCAAAACAGCAGAGTGTCTCCATTGGACACAGAG 312
 Qy 301 TGGGAATTCCAAAGTATGGGCACCTAG 327

QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGACAACAGAGAG 300
 Db 257 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGACAACAGAGAG 316
 QY 301 TGGGAATTCCAAAGATGGGCACTAG 327
 Db 317 TGGGAATTCCAAAGATGGGCACTAG 343

RESULT 22
 BI858425 549 bp mRNA linear EST 10-OCT-2001
 LOCUS 603386437F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5395281 5',
 DEFINITION mRNA sequence.
 ACCESSION BI858425
 VERSION BI858425.1 GI:15999172
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 549)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12007 row: i column: 10
 High quality sequence stop: 525.
 FEATURES Location/Qualifiers
 1..549
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5395281"
 /tissue_type="mammary adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_87"
 /note="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dr primed.
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 327; DB 3; Length 549;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGCGCAGCATGTGGATATACCCGAGCGGCAACCAACAGCGCGCGGCAAGAAG 60
 Db 1 ATGCGCGCAGCATGTGGATATACCCGAGCGGCAACCAACAGCGCGCGGCAAGAAG 60
 QY 61 CGCTTTCAAGTGAAGATGCAATGCAATGAGTCTTGGCCCTGGGATATTGGTTGAT 120
 Db 61 CGCTTTCAAGTGAAGATGCAATGCAATGAGTCTTGGCCCTGGGATATTGGTTGAT 120
 QY 121 AACTGTGCCATCTCGAGGAACCAATATGATCTTTGATAGATGCTCAAGCTAACCCAG 180
 Db 121 AACTGTGCCATCTCGAGGAACCAATATGATCTTTGATAGATGCTCAAGCTAACCCAG 180
 QY 181 GCGTCCGCTACTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTAC 240
 Db 181 GCGTCCGCTACTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTAC 240

QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGACAACAGAGAG 300
 Db 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGACAACAGAGAG 300
 QY 301 TGGGAATTCCAAAGATGGGCACTAG 327
 Db 301 TGGGAATTCCAAAGATGGGCACTAG 327

RESULT 23
 BU955646 550 bp mRNA linear EST 21-OCT-2002
 LOCUS AGENCOURT 10612538 NIH_MGC 126 Homo sapiens cDNA clone
 DEFINITION IMAGE:6727878 5', mRNA sequence.
 ACCESSION BU955646
 VERSION BU955646.1 GI:24185218
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 550)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM3048 row: j column: 05
 High quality sequence stop: 520.
 FEATURES Location/Qualifiers
 1..550
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6727878"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH_MGC_126"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggccgctcggc); Double-stranded cDNA was
 prepared from a pool of 40 cell line polyA+ RNAs (bladder
 - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
 kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
 salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
 adaptors were used in cloning as follows:
 5'-AAGCAGTGTATCAACGACGATGGCATACGCGCGG-3' and
 5'-ATTCTAGAGCCGAGCGCGGACATG-dr(30)NN-3' Full-length
 enriched library was constructed using the Clontech
 Creator SMART kit and size-selected to contain the 0.5-1
 kb size fraction (other fractions present in NIH_MGC.127
 and NIH_MGC.128). Library created in the laboratory of T.
 Uedlin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
 Library."

ORIGIN
 Query Match 100.0%; Score 327; DB 5; Length 550;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGCGCAGCATGTGGATATACCCGAGCGGCAACCAACAGCGCGCGGCAAGAAG 60
 Db 17 ATGCGCGCAGCATGTGGATATACCCGAGCGGCAACCAACAGCGCGCGGCAAGAAG 76

and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 555;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGAGGATGGATGGATACCCCGAGCGGCACCAACAGCGGCGGCAAGAAG 60
Db 13 ATGGCGGAGGATGGATGGATACCCCGAGCGGCACCAACAGCGGCGGCAAGAAG 72
Qy 61 CGCTTTGAAGTCAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 120
Db 73 CGCTTTGAAGTCAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 132
Qy 121 AACTGTGCATCTGCAGGAACACATATGATCTTTGCATAGATGTCAAGCTAACAG 180
Db 133 AACTGTGCATCTGCAGGAACACATATGATCTTTGCATAGATGTCAAGCTAACAG 192
Qy 181 CGCTCCGCTACTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 193 CGCTCCGCTACTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTTCAC 252
Qy 241 TTCCACTGCATCTCTCGCTGGCTCAAAACAGCAGAGTGTGTCCATTGGACACAGAGAG 300
Db 253 TTCCACTGCATCTCTCGCTGGCTCAAAACAGCAGAGTGTGTCCATTGGACACAGAGAG 312
Qy 301 TGGGAATTCAAAAGTATGGCACTAG 327
Db 313 TGGGAATTCAAAAGTATGGCACTAG 339

RESULT 26

BU601080 555 bp mRNA linear EST 20-SEP-2002
LOCUS AGENCOURT 10058991 NIH_MGC 142 Homo sapiens cDNA clone
DEFINITION IMAGE:6494946 5', mRNA sequence.

ACCESSION BU601080

VERSION BU601080.1 GI:23252839

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 555)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: NCI

CDNA Library Preparation: Michael Brownstein Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2671 row: p column: 19

High quality sequence stop: 510.

FEATURES

source

1..555

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6494946"

/cisse_type="mixed (pool of 40 RNAs)"

/lab_hosts="DH10B (Tl-phage-resistant)"

/clone_lib="NIH_MGC_142"

/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccgctcgcc); Double-stranded cDNA was

prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:

5'-AAGCAGTGGTATCAACGAGCGGCACATG-dt(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH_MGC_141). Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 555;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGAGGATGGATGGATACCCCGAGCGGCACCAACAGCGGCGGCAAGAAG 60
Db 22 ATGGCGGAGGATGGATGGATACCCCGAGCGGCACCAACAGCGGCGGCAAGAAG 81
Qy 61 CGCTTTGAAGTCAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 120
Db 82 CGCTTTGAAGTCAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 141
Qy 121 AACTGTGCATCTGCAGGAACACATATGATCTTTGCATAGATGTCAAGCTAACAG 180
Db 142 AACTGTGCATCTGCAGGAACACATATGATCTTTGCATAGATGTCAAGCTAACAG 201
Qy 181 CGCTCCGCTACTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 202 CGCTCCGCTACTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTTCAC 261
Qy 241 TTCCACTGCATCTCTCGCTGGCTCAAAACAGCAGAGTGTGTCCATTGGACACAGAGAG 300
Db 262 TTCCACTGCATCTCTCGCTGGCTCAAAACAGCAGAGTGTGTCCATTGGACACAGAGAG 321
Qy 301 TGGGAATTCAAAAGTATGGCACTAG 327
Db 322 TGGGAATTCAAAAGTATGGCACTAG 348

RESULT 27

BU954591 557 bp mRNA linear EST 21-OCT-2002
LOCUS AGENCOURT 10610692 NIH_MGC 126 Homo sapiens cDNA clone
DEFINITION IMAGE:6726227 5', mRNA sequence.

ACCESSION BU954591

VERSION BU954591.1 GI:24184163

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 557)

NIH-MGC <http://mgi.nci.nih.gov/>.

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: NCI

CDNA Library Preparation: Michael Brownstein Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM3044 row: e column: 10

High quality sequence stop: 469.

FEATURES
source
 Location/Qualifiers
 1. .557
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6726227"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH_MGC_126"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgccctcgcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%) 5' and 3' adaptors were used in cloning as follows:
 5'-AAGCAGTGGTATCAACGAGATGGCCATTACGGCCGG-3' and 5'-ATTCTAGAGCGGCGGCGGACATG-DT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 327; DB 5; Length 557;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGGATGGATGGATACCCGAGCGGCACCAACAGCGCGGGCAAGAAG 60
 DB 22 ATGGCGGCGGATGGATGGATACCCGAGCGGCACCAACAGCGCGGGCAAGAAG 81
 QY 61 CGCTTTGAAGTGAAGTGAAGTGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 120
 DB 82 CGCTTTGAAGTGAAGTGAAGTGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 141
 QY 121 AACTGTGCCATCTGCAGGAACACATTATGGATCTTTGCATAGATGTCAGCTTAACCAAG 180
 DB 142 AACTGTGCCATCTGCAGGAACACATTATGGATCTTTGCATAGATGTCAGCTTAACCAAG 201
 QY 181 GCGTCGCTACTTCAGAGAGTGTACTGTCGATGGGAGTCTGTAACCATGCTTTTCAC 240
 DB 202 GCGTCGCTACTTCAGAGAGTGTACTGTCGATGGGAGTCTGTAACCATGCTTTTCAC 261
 QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTTGTGTCATTGGACACAGAGAG 300
 DB 262 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTTGTGTCATTGGACACAGAGAG 321
 QY 301 TGGGAATTCCTCAAGATGATGGCACTAG 327
 DB 322 TGGGAATTCCTCAAGATGATGGCACTAG 348

RESULT 28
 CD388268
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 558)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

FEATURES
source
 Location/Qualifiers
 1. .557
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6726227"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH_MGC_126"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggcgccctcgcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%) 5' and 3' adaptors were used in cloning as follows:
 5'-AAGCAGTGGTATCAACGAGATGGCCATTACGGCCGG-3' and 5'-ATTCTAGAGCGGCGGCGGACATG-DT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 100.0%; Score 327; DB 6; Length 558;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGGATGGATGGATACCCGAGCGGCACCAACAGCGCGGGCAAGAAG 60
 DB 32 ATGGCGGCGGATGGATGGATACCCGAGCGGCACCAACAGCGCGGGCAAGAAG 91
 QY 61 CGCTTTGAAGTGAAGTGAAGTGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 120
 DB 92 CGCTTTGAAGTGAAGTGAAGTGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 151
 QY 121 AACTGTGCCATCTGCAGGAACACATTATGGATCTTTGCATAGATGTCAGCTTAACCAAG 180
 DB 152 AACTGTGCCATCTGCAGGAACACATTATGGATCTTTGCATAGATGTCAGCTTAACCAAG 211
 QY 181 GCGTCGCTACTTCAGAGAGTGTACTGTCGATGGGAGTCTGTAACCATGCTTTTCAC 240
 DB 212 GCGTCGCTACTTCAGAGAGTGTACTGTCGATGGGAGTCTGTAACCATGCTTTTCAC 271
 QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTTGTGTCATTGGACACAGAGAG 300
 DB 272 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTTGTGTCATTGGACACAGAGAG 331
 QY 301 TGGGAATTCCTCAAGATGATGGCACTAG 327
 DB 332 TGGGAATTCCTCAAGATGATGGCACTAG 358

RESULT 29
 CD388268
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 559)
 NIH-MGC http://mgi.nci.nih.gov/

COMMENT
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Dr. Jamie Thompson, University of WI
 cDNA Library Preparation: Gina Zastrow-Hayes
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 DNA Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDR80 row: h column: 04
 High quality sequence start: 13
 High quality sequence stop: 558.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic trophoblasts, made from WA01 stem cells"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_173"
 /note="Vector: pDNR201; Site 1: attP2; Site 2: attP1;
 LIBR PRIMING - oligo dr; METHOD - full-length enriched;
 LIBR PROVIDER - Bradfield"

TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: dsgerbo@mail.nih.gov Tissue Procurement: Professor Miklos Palkovits cDNA Library Preparation: Michael Brownstein / Ted Usdin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDCM264 row: n column: 01 High quality sequence stop: 543.		
FEATURES	Location/Qualifiers		
source	1..559 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:30719640" /tissue_type="Human Brain - Cerebellar Cortex" /lab_host="DH10B Tona" /clone_lib="NIH_MGC 228" /notes="Organ: brain/CNS; Vector: pDNR-LIB; Site 1: SfiI (directional); Site 2: SfiI (directional); Library is oligo-dT primed and directionally cloned.5' and 3' adaptors were used in cloning as follows: 5'-AAGCAGGTGATCAACGACAGTGCCTATTACGCGGG-3'5'-ATTCTAGAGG CCGAGCGGCGCATG-D(T)3N-IN-3. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected for >0.5kb with an average insert size of 1.2kb Library created in the laboratory of Jonathan Kuo and Ted Usdin."		
ORIGIN	Query Match 100.0%; Score 327; DB 7; Length 559; Best Local Similarity 100.0%; Pred. No. 6.6e-175; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	ATGCGGCACGGATGGATGTGGATATACCCCGAGCGGCACCAACGCGCGCGGCGCAAGAAG	60
Db	23	ATGCGGCACGGATGGATGTGGATATACCCCGAGCGGCACCAACGCGCGCGGCGCAAGAAG	82
Qy	61	CGCTTTGAAGTGAAGAAGTGGATGCAATGTCAGTACCCCTCTGGGCCTGGGATATGTGGTTGAT	120
Db	83	CGCTTTGAAGTGAAGAAGTGGATGCAATGTCAGTACCCCTCTGGGCCTGGGATATGTGGTTGAT	142
Qy	121	AACGTGTCCCATCTGCAGGAACCAATATGGAATCTTTGCATAGAAATGCTCAAGCTAACCGAG	180
Db	143	AACGTGTCCCATCTGCAGGAACCAATATGGAATCTTTGCATAGAAATGCTCAAGCTAACCGAG	202
Qy	181	GCCTCCGCTACTTCAGAAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCAC	240
Db	203	GCCTCCGCTACTTCAGAAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCAC	262
Qy	241	TTCCACTGGATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACACACAGAGAG	300
Db	263	TTCCACTGGATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACACACAGAGAG	322
Qy	301	TGGGAATTCCAAAGATGGGCCTAG	327
Db	323	TGGGAATTCCAAAGATGGGCCTAG	349
RESULT 30			
CD175085			
LOCUS	CD175085	562 bp	mRNA linear EST 19-MAY-2003
DEFINITION	AGENCOURT_13976103 NIH_MGC_172 Homo sapiens cDNA 5', mRNA sequence.		
ACCESSION	CD175085		
VERSION	CD175085.1 GI:30859303		

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 563)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2901 row: g column: 04
High quality sequence stop: 531.

FEATURES
Location/Qualifiers
1..563
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6652636"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (TI-phage-resistant)"
/clone_lib="NIH MGC 126"
/notes="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcgctcgcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGAGTGGCCATTACGCGCGG-3' and
5'-ATTCTAGAGCGGCGGCGGCGGACATG-DT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5-1
kb size fraction (other fractions present in NIH MGC 127
and NIH MGC 128). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 100.0%; Score 327; DB 5; Length 563;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCGCGCAGCGATGGATGGATGATACCCGAGCGGCACCAACAGCGCGCGGCGGCAAGAAG 60
Db 32 ATGCGCGCAGCGATGGATGGATGATACCCGAGCGGCACCAACAGCGCGCGGCGGCAAGAAG 91
Qy 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 92 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 151
Qy 121 AACTGTGCCATCTCGAGGACCAATATGATGATCTTGGGCTGGGATATTTGGTTGAT 180
Db 152 AACTGTGCCATCTCGAGGACCAATATGATGATCTTGGGCTGGGATATTTGGTTGAT 211
Qy 181 CGCTCCGCTACTTCAGAGAGTGTACTGTCCATGGGAGTCTGTAAACCATGCTTTTTCAC 240
Db 212 CGCTCCGCTACTTCAGAGAGTGTACTGTCCATGGGAGTCTGTAAACCATGCTTTTTCAC 271
Qy 241 TTCCATGTCATCTCTCGCTGCTCAAAACACGACGAGTGTCTCATTTGGACAAACAGAGAG 300
Db 272 TTCCATGTCATCTCTCGCTGCTCAAAACACGACGAGTGTCTCATTTGGACAAACAGAGAG 331
Qy 301 TGGGAATTCGAAAGTATGGCACTAG 327

Db 332 TGGGAATTCGAAAGTATGGCACTAG 358

RESULT 32
BUS97842
LOCUS
DEFINITION
5', mRNA sequence.
ACCESSION
BUS97842
VERSION
BUS97842.1 GI:23249601
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 570)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2636 row: h column: 12
High quality sequence stop: 478.

FEATURES
Location/Qualifiers
1..570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6456347"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (TI-phage-resistant)"
/clone_lib="NIH MGC 142"
/notes="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcgctcgcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
used in cloning as follows:
5'-AAGCAGTGGTATCAACGAGTGGCCATTACGCGCGG-3' and
5'-ATTCTAGAGCGGCGGCGGCGGACATG-DT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the >0.5 kb
size fraction (other fractions present in NIH MGC 141).
Library created in the laboratory of M. Brownstein (NIMH,
NIH). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 100.0%; Score 327; DB 5; Length 570;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCGCGCAGCGATGGATGGATGATACCCGAGCGGCACCAACAGCGCGCGGCGGCAAGAAG 60
Db 32 ATGCGCGCAGCGATGGATGGATGATACCCGAGCGGCACCAACAGCGCGCGGCGGCAAGAAG 91
Qy 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 92 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 151
Qy 121 AACTGTGCCATCTCGAGGACCAATATGATGATCTTGGGCTGGGATATTTGGTTGAT 180
Db 152 AACTGTGCCATCTCGAGGACCAATATGATGATCTTGGGCTGGGATATTTGGTTGAT 211

QY 181 GCGTCGGCTACTTTCAGAGAGTGTACTGTCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
 |||||
 Db 212 GCGTCGGCTACTTTCAGAGAGTGTACTGTCGATGGGAGTCTGTAAACCATGCTTTTCAC 271
 |||||
 QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGCCATTGGACAACAGAGAG 300
 |||||
 Db 272 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGCCATTGGACAACAGAGAG 331
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 QY 301 TGGGAATTCAAAAGTATGGGCACCTAG 327
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 Db 332 TGGGAATTCAAAAGTATGGGCACCTAG 358
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RESULT 33
 BU533405
 LOCUS BU533405 573 bp mRNA linear EST 13-SEP-2002
 DEFINITION AGENCOURT.10197895 NIH_MGC_126 Homo sapiens cDNA clone
 IMAGE:6559746 5', mRNA sequence.

ACCESSION BU533405
 VERSION BU533405.1 GI:22843846

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.

1 (bases 1 to 573)

REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

AUTHORS Contact: Robert Strausberg, Ph.D.

TITLE Email: cgapbs-rc@mail.nih.gov

JOURNAL Tissue Procurement: NCI

COMMENT cDNA Library Preparation: Michael Brownstein Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2731 row: h column: 18

High quality sequence stop: 544.

Location/Qualifiers

FEATURES

source

1..573
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6559746"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH MGC 126"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggccgcttcggc); Double-stranded cDNA was
 prepared from a pool of 40 cell line polyA+ RNAs (bladder
 - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
 kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
 salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
 adaptors were used in cloning as follows:
 5'-AAGCAGTGTATCAACGAGTGGCCATTACGGCGGG-3' and
 5'-ATTCTAGAGCGGCGCGCGCATG-dt(30)NN-3'. Full-length
 enriched library was constructed using the Clontech
 Creator SMART kit and size-selected to contain the 0.5-1
 kb size fraction (other fractions present in NIH_MGC_127
 and NIH_MGC_128). Library created in the laboratory of T.
 Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 573;
 Best Local Similarity 100.0%; Pred. No. 6.6e-175;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGCACCAACAGCGGCGCGGCAAGAG 60
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 Db 38 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGCACCAACAGCGGCGCGGCAAGAG 97
 |||||
 QY 61 CGCTTTGAAGTGAAAAAGTGGAAATCAGTAGCCCTCTGGGCCCTGGGATATTGTGTTGAT 120
 |||||
 Db 98 CGCTTTGAAGTGAAAAAGTGGAAATCAGTAGCCCTCTGGGCCCTGGGATATTGTGTTGAT 157
 |||||
 QY 121 AACTGTGCCATCTGCAGGAACCCACATTATGGATCTTTGCATAGATGTCAAGCTAACACAG 180
 |||||
 Db 158 AACTGTGCCATCTGCAGGAACCCACATTATGGATCTTTGCATAGATGTCAAGCTAACACAG 217
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 QY 181 CGCTCCGCTACTTTCAGAAAGTGTACTGTGCGATGGGAGTGTGTAACCATGCTTTTCAC 240
 |||||
 Db 218 CGCTCCGCTACTTTCAGAAAGTGTACTGTGCGATGGGAGTGTGTAACCATGCTTTTCAC 277
 |||||
 QY 241 TTCACATGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGTCATTGGACAACAGAGAG 300
 |||||
 Db 278 TTCACATGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGTCATTGGACAACAGAGAG 337
 |||||
 QY 301 TGGGAATTCAAAAGTATGGGCACCTAG 327
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 Db 338 TGGGAATTCAAAAGTATGGGCACCTAG 364
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RESULT 34

BP308845

LOCUS BP308845

DEFINITION BP308845 Sugano cDNA library, brain Homo sapiens cDNA clone

NR806593, mRNA sequence.

ACCESSION BP308845

VERSION BP308845.1 GI:52237818

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominiidae; Homo.

1 (bases 1 to 581)

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

source

1..581

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="NR806593"

/tissue_type="brain"

/clone_lib="Sugano cDNA library, brain"

ORIGIN

Query Match 100.0%; Score 327; DB 3; Length 581;

Best Local Similarity 100.0%; Pred. No. 6.6e-175;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGCACCAACAGCGGCGCGGCAAGAG 60

Db 14 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGCACCAACAGCGGCGCGGCAAGAG 73

QY 61 CGCTTTGAAGTGAAAAAGTGGAAATCAGTAGCCCTCTGGGCCCTGGGATATTGTGTTGAT 120

Db 74 CGCTTTGAAGTGAAAAAGTGGAAATCAGTAGCCCTCTGGGCCCTGGGATATTGTGTTGAT 133

```

QY 121 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTGGCATAGATGTCAAGCTAACCG 180
Db 134 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTGGCATAGATGTCAAGCTAACCG 193
QY 181 GCGTCCGCTACTTTCAGAAAGTGTACTGTCCGATGGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 194 GCGTCCGCTACTTTCAGAAAGTGTACTGTCCGATGGGGAGTCTGTAAACCATGCTTTTCAC 253
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGGACAAACAGAG 300
Db 254 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGGACAAACAGAG 313
QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
Db 314 TGGGAATTCAAAAGTATGGGCACTAG 340

RESULT 35
BP317451 583 bp mRNA linear EST 17-SEP-2004
LOCUS BP317451 Sugano cDNA library, pericardium Homo sapiens cDNA clone
DEFINITION PCD03725, mRNA sequence.
ACCESSION BP317451
VERSION BP317451.1 GI:52246426
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane-dai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1. 583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PCD03725"
/tissue_type="pericardium"
/clone_lib="Sugano cDNA library, pericardium"

ORIGIN
Query Match 100.0%; Score 327; DB 3; Length 583;
Best Local Similarity 100.0%; Pred. No. 6.6e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCGGCAAGAG 60
Db 12 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCGGCAAGAG 71
QY 61 CGCTTTGAAGTGAAAGAGTGAAGTGCAGTAGCCCTCTGGGCGCTGGGATATTGTGGTTGAT 120
Db 72 CGCTTTGAAGTGAAAGAGTGAAGTGCAGTAGCCCTCTGGGCGCTGGGATATTGTGGTTGAT 131
QY 121 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTGGCATAGATGTCAAGCTAACCG 180
Db 132 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTGGCATAGATGTCAAGCTAACCG 191
QY 181 GCGTCCGCTACTTTCAGAAAGTGTACTGTCCGATGGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 192 GCGTCCGCTACTTTCAGAAAGTGTACTGTCCGATGGGGAGTCTGTAAACCATGCTTTTCAC 251
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGGACAAACAGAG 300

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Db 252 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGTCCATTGGGACAAACAGAG 311
QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
Db 312 TGGGAATTCAAAAGTATGGGCACTAG 338

RESULT 36
BG705958 616 bp mRNA linear EST 07-MAY-2001
LOCUS BG705958 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4792099 5',
DEFINITION mRNA sequence.
ACCESSION BG705958
VERSION BG705958.1 GI:13980825
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 616)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10669 row: 1 column: 20
High quality sequence stop: 591.
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1. 616
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4792099"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtccag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN
Query Match 100.0%; Score 327; DB 2; Length 616;
Best Local Similarity 100.0%; Pred. No. 6.7e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCGGCAAGAG 60
Db 19 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCGGCAAGAG 78
QY 61 CGCTTTGAAGTGAAAGAGTGAAGTGCAGTAGCCCTCTGGGCGCTGGGATATTGTGGTTGAT 120
Db 79 CGCTTTGAAGTGAAAGAGTGAAGTGCAGTAGCCCTCTGGGCGCTGGGATATTGTGGTTGAT 138
QY 121 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTGGCATAGATGTCAAGCTAACCG 180
Db 139 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTGGCATAGATGTCAAGCTAACCG 198

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QY 181 GCGTCGGTACTTTCAGAGAGTGTAATGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
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Db 199 GCGTCGGTACTTTCAGAGAGTGTAATGCGATGGGAGTCTGTAAACCATGCTTTTCAC 258
    |||
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTCCTATTCGACACAGAGAG 300
    |||
Db 259 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTCCTATTCGACACAGAGAG 318
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QY 301 TGGGAATTCCTCAAAAGTATGGGCACTAG 327
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Db 319 TGGGAATTCCTCAAAAGTATGGGCACTAG 345
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RESULT 37
BG503311
LOCUS BG503311 NIH_MGC_61 736 bp mRNA linear EST 27-MAR-2001
DEFINITION 602550721F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4658381 5',
    mRNA sequence.
ACCESSION BG503311
VERSION BG503311.1 GI:13464828
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 736)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

```

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CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1452 row: i column: 06
High quality sequence stop: 515.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_61"
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggccgctcgcc); Site:2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCGGCATG-dT(30)BN-3',
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

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FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_61"
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggccgctcgcc); Site:2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCGGCATG-dT(30)BN-3',
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

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ORIGIN

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Query Match 100.0%; Score 327; DB 2; Length 736;
Best Local Similarity 100.0%; Pred. No. 6.7e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCGGAGGATGGATGGATATCCCGAGCGGCACCAACAGCGCGCGGGAAGAG 60
    |||
Db 12 ATGGCGGAGGATGGATGGATATCCCGAGCGGCACCAACAGCGCGCGGGAAGAG 71
    |||

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QY 61 CGCTTTGAAGTGAAAAAGTCAGTAGCCCTCTCGGCTCGGATATTGTGTTGAT 120
    |||
Db 72 CGCTTTGAAGTGAAAAAGTCAGTAGCCCTCTCGGCTCGGATATTGTGTTGAT 131
    |||
QY 121 AACTGTGCCATCTCGCAGCAACACATTATGATCTTTGCATAGATGTCAAGCTAACAG 180
    |||
Db 132 AACTGTGCCATCTCGCAGCAACACATTATGATCTTTGCATAGATGTCAAGCTAACAG 191
    |||
QY 181 CGCTCCGCTACTTTCAGAAAGTGTAATGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
    |||
Db 192 CGCTCCGCTACTTTCAGAAAGTGTAATGCGATGGGAGTCTGTAAACCATGCTTTTCAC 251
    |||
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTCCTATTCGACACAGAGAG 300
    |||
Db 252 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTCCTATTCGACACAGAGAG 311
    |||
QY 301 TGGGAATTCCTCAAAAGTATGGGCACTAG 327
    |||
Db 312 TGGGAATTCCTCAAAAGTATGGGCACTAG 338
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RESULT 38

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BG533420
LOCUS BG533420 801 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT 10197966 NIH_MGC_126 Homo sapiens cDNA clone
    IMAGE:6559775 5', mRNA sequence.
ACCESSION BG533420
VERSION BG533420.1 GI:22843861
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 801)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2731 row: i column: 23
High quality sequence stop: 551.
Location/Qualifiers
1..801
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:6559775"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_126"
/notes="Vector: pDNR-LIB; Site:1: SfiI (ggccattatggcc);
Site:2: SfiI (ggccgctcgcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGAGCGGCATTCAGCGCGCG-3' and
5'-ATTCTAGAGCCGAGCGCGGCATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5-1
kb size fraction (other fractions present in NIH_MGC_127
and NIH_MGC_128). Library created in the laboratory of T.

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FEATURES

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source
1..801
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:6559775"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_126"
/notes="Vector: pDNR-LIB; Site:1: SfiI (ggccattatggcc);
Site:2: SfiI (ggccgctcgcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGAGCGGCATTCAGCGCGCG-3' and
5'-ATTCTAGAGCCGAGCGCGGCATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5-1
kb size fraction (other fractions present in NIH_MGC_127
and NIH_MGC_128). Library created in the laboratory of T.

```

Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN	Query Match	100.0%;	Score 327;	DB 5;	Length 801;
	Best Local Similarity	100.0%;	Pred. No. 6.8e-175;		
	Matches 327;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACGCGCGGGGCAAGAAG	60		
DB	44	ATGGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACGCGCGGGGCAAGAAG	103		
QY	61	CGCTTTGAAGTGA AAAAGTGGAAATGCAGTAGCCCTCTGGGCGCTGGGATATTGTGGTTGAT	120		
DB	104	CGCTTTGAAGTGA AAAAGTGGAAATGCAGTAGCCCTCTGGGCGCTGGGATATTGTGGTTGAT	163		
QY	121	AACGTGCGCCATCTGCAGGAACCAATTATGGATCTTTGGCATAGAAATGTCAAGCTTAACCAAG	180		
DB	164	AACGTGCGCCATCTGCAGGAACCAATTATGGATCTTTGGCATAGAAATGTCAAGCTTAACCAAG	223		
QY	181	CGGTCCGCTACTTTCAGAAAGATGTACTGTCCGATGGGAGTCTCTGAACCATGCTTTTTCAC	240		
DB	224	CGGTCCGCTACTTTCAGAAAGATGTACTGTCCGATGGGAGTCTCTGAACCATGCTTTTTCAC	283		
QY	241	TTCCACTTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG	300		
DB	284	TTCCACTTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG	343		
QY	301	TGGGAATTCCAAAAGTATGGGCACCTAG	327		
DB	344	TGGGAATTCCAAAAGTATGGGCACCTAG	370		

RESULT 39
 BU959349
 LOCUS
 DEFINITION
 BU959349 845 bp mRNA linear EST 21-OCT-2002
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 1 (bases 1 to 845)
 NTH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
Plate: LLM3067 row: m column: 19
High quality sequence stop: 424.
FEATURES
      Location/Qualifiers
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              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:6737564"
              /tissue_type="mixed (pool of 40 RNAs)"
              /lab_host="DH10B (T1-phage-resistant)"
              /clone_lib="NIH MSC 127"
              /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattaggcc);
              Site 2: SfiI (ggcgctctggcc); Double-stranded cDNA was
              prepared from a pool of 40 cell line polyA+ RNAs (bladder

```

- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGACGAGTGGCATTCACGGCGG-3' and 5'-ATTCTAGACGCGGCGCGCATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH_MGC_126 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN		Query Match Best Local Similarity Matches 327; Conservative 0;	100.0%; 100.0%; 327;	Score 327; Pred. No..6e-175; Mismatches 0;	DB 5; Indels 0;	Length 845; Gaps 0;
Qy	1	ATGGCGCAGGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG	60			
Dd	22	ATGGCGCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG	81			
Qy	61	CGCTTTCAAAGTGA AAAAGTGGAATGCAGTAGCCCTCTGGGCGCTGGGATATTGTGGTTGAT	120			
Dd	82	CGCTTTGAGAGTGA AAAAGTGGAATGCAGTAGCCCTCTGGGCGCTGGGATATTGTGGTTGAT	141			
Qy	121	AACTGTGCCATCTCGAGAAACCA CATTATGGATCTTTTGCATAGATAATGTCAAGCTAACCAAG	180			
Dd	142	AACTGTGCCATCTCGAGAAACCA CATTATGGATCTTTTGCATAGATAATGTCAAGCTAACCAAG	201			
Qy	181	GCGTCCGCTACTTCAGAGAGAGTGACTGTCCGATGGGAGTCTGTAAACAATGCTTTTTCAC	240			
Dd	202	GCGTCCGCTACTTCAGAGAGAGTGACTGTCCGATGGGAGTCTGTAAACAATGCTTTTTCAC	261			
Qy	241	TTCCACTTGCATCTCTCGCTGGCTCAAAAACAGCACAGGTGTGTCCAATTGGACAACAGAGAG	300			
Dd	262	TTCCACTTGCATCTCTCGCTGGCTCAAAAACAGCACAGGTGTGTCCAATTGGACAACAGAGAG	321			
Qy	301	TGGGAATTCCAAAAGTATGGGCAC TAG	327			
Dd	322	TGGGAATTCCAAAAGTATGGGCAC TAG	348			

RESULT 40	886 bp	linear	EST 21-MAR-2000
LOCUS	886 bp	linear	EST 21-MAR-2000
DEFINITION	886 bp	linear	EST 21-MAR-2000
ACCESSION	886 bp	linear	EST 21-MAR-2000
VERSION	886 bp	linear	EST 21-MAR-2000
KEYWORDS	886 bp	linear	EST 21-MAR-2000
SOURCE	886 bp	linear	EST 21-MAR-2000
ORGANISM	886 bp	linear	EST 21-MAR-2000
REFERENCE	886 bp	linear	EST 21-MAR-2000
AUTHORS	886 bp	linear	EST 21-MAR-2000
TITLE	886 bp	linear	EST 21-MAR-2000
JOURNAL	886 bp	linear	EST 21-MAR-2000
COMMENT	886 bp	linear	EST 21-MAR-2000

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FEATURES          source          Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:4652028"
/tissue_type="choriocarcinoma"
/lab_host="NIH MGC 21"
/clone_lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

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Query Match      100.0%; Score 327; DB 2; Length 886;
Best Local Similarity 100.0%; Pred. No. 6.8e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGCGAGTGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAG 60
Db 7 ATGGCGGCGAGTGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAG 66
Qy 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 120
Db 67 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 126
Qy 121 AACTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTAAC 180
Db 127 AACTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTAAC 186
Qy 181 CGCTCCGCTACTTCAGAAAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 187 CGCTCCGCTACTTCAGAAAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
Qy 241 TTCCACTGCATCTCTCGCTGGCTCAAAACAGACAGAGTGTCTCCATTGGACAAACAGAG 300
Db 247 TTCCACTGCATCTCTCGCTGGCTCAAAACAGACAGAGTGTCTCCATTGGACAAACAGAG 306
Qy 301 TGGGAATTCCAAAGTATGGCACTAG 327
Db 307 TGGGAATTCCAAAGTATGGCACTAG 333
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RESULT 41

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BM459634
LOCUS      BM459634
DEFINITION AGENCOURT_6417786 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534260
5', mRNA sequence.
ACCESSION  BM459634
VERSION     BM459634.1 GI:18508674
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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http://image.llnl.gov
Plate: L1AM12220 row: h column: 05
High quality sequence stop: 684.

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FEATURES          source          Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:5534260"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
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ORIGIN

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Query Match      100.0%; Score 327; DB 3; Length 904;
Best Local Similarity 100.0%; Pred. No. 6.8e-175;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGCGAGTGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAG 60
Db 10 ATGGCGGCGAGTGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAG 69
Qy 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 120
Db 70 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGAT 129
Qy 121 AACTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTAAC 180
Db 130 AACTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTAAC 189
Qy 181 CGCTCCGCTACTTCAGAAAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 190 CGCTCCGCTACTTCAGAAAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCAC 249
Qy 241 TTCCACTGCATCTCTCGCTGGCTCAAAACAGACAGAGTGTCTCCATTGGACAAACAGAG 300
Db 250 TTCCACTGCATCTCTCGCTGGCTCAAAACAGACAGAGTGTCTCCATTGGACAAACAGAG 309
Qy 301 TGGGAATTCCAAAGTATGGCACTAG 327
Db 310 TGGGAATTCCAAAGTATGGCACTAG 336
```

RESULT 42

```

BM459634
LOCUS      BM459634
DEFINITION AGENCOURT_7575192 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6049202
5', mRNA sequence.
ACCESSION  BM459634
VERSION     BM459634.1 GI:20398138
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
```

Plate: L1AM13299 row: h column: 03

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 12:22:08 ; Search time 368.547 Seconds
(without alignments)
5913.368 Million cell updates/sec

Title: US-09-541-462B-1

Perfect score: 327

Sequence: 1 atggcgagcgatggatgt.....tccaaagtatgggcactag 327

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 12

Total number of hits satisfying chosen parameters: 116703

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	327	3	AA096882 Nucleotide
2	327	100.0	482	3	AA03896 Human sec
3	327	100.0	506	12	AD087496 Human tum
4	327	100.0	506	12	AD087156 Human tum
5	327	100.0	506	13	AD084881 Human tum
6	327	100.0	508	3	AA074978 Human encod
7	327	100.0	508	13	ACN40951 Tumour-as
8	325	99.4	476	9	ACH29979 Human tes
9	321	98.2	3726	13	AD080913 Human tes
10	321	98.2	4543	11	ACN90161 Breast ca
11	320	97.9	503	12	AD092179 Human aut
12	308	94.2	4476	5	ABV25615 Human pro
13	296	90.5	311	14	ACL57420 Human col
14	296	90.5	3484	12	ADf42703 Human tes
15	296	90.5	3484	12	ADq18564 Human sof
16	296	90.5	3484	13	ADQ08065 Human SPA
17	296	90.5	5111	10	ADB75558 Prostate
18	296	90.5	5371	12	ADQ23032 Human sof
19	267	81.7	5347	6	AAS94844 Human DNA

C	20	251	76.8	502	14	ADY78665	Ady78665 Human cdn
	21	249	76.1	3208	4	AAD12859	Aad12859 Human nov
	22	209	63.9	509	5	AAS86845	Aas86845 DNA encod
	23	170	52.0	402	3	AAC06296	Aac06296 Human sec
	24	170	52.0	439	9	ACH27559	Ach27559 Human adu
	25	170	52.0	1482	3	AAC75216	Aac75216 Human ORF
	26	166	50.8	380	8	ABX39512	Abx39512 Bovine ES
	27	149	45.6	666	5	AAS86844	Aas86844 DNA encod
	28	147	45.0	398	5	AAS86841	Aas86841 DNA encod
	29	131	40.1	358	5	AAS86842	Aas86842 DNA encod
	30	131	40.1	386	5	AAS86843	Aas86843 DNA encod
	31	99	30.3	416	5	AAS86840	Aas86840 DNA encod
	32	99	30.3	812	6	ABQ54871	Abq54871 Human ova
	33	99	30.3	1478	12	ADJ72047	Adj72047 Human PMM
	34	90	27.5	346	4	AAL11142	Aal11142 Human bre
	35	90	27.5	353	4	AAL18905	Aal18905 Human bre
	36	89	27.5	415	11	ACN81343	Acn81343 Breast ca
	37	89	27.2	11301	4	AAK71591	Aak71591 Human imm
	38	78	23.9	439	6	ABQ99527	Abq99527 Human cod
	39	65	19.9	4099	5	AAS86847	Aas86847 DNA encod
	40	54	16.5	254	2	AAT26036	Aat26036 Human gen
	41	50	15.3	504	3	AAA74980	Aaa74980 DNA encod
	42	50	15.3	539	5	AAH97860	Aah97860 Murine 7-
	43	50	15.3	557	5	AAH97861	Aah97861 Murine 7-
	44	50	15.3	586	5	AAH97862	Aah97862 Murine 7-
	45	40	12.2	416	4	AAI89292	Aai89292 Human pol

ALIGNMENTS

RESULT 1

AAA96882

ID AAA96882 standard; DNA; 327 BP.

XX AC AAA96882;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of human ring finger protein ROC1.

XX ROC1; ROC2; cullin; ring finger protein; APC11; APC complex; SCF pathway;
XX cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation;
XX tumour; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..327

FT /*tag= a

FT /product= "ROC1"

XX WO200058472-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US008592.

XX 31-MAR-1999; 99US-0127261P.

XX 22-NOV-1999; 99US-0166927P.

XX (UYNC-) UNIV NORTH CAROLINA.

XX Xiong Y, Ohta T;

XX WPI; 2000-647235/62.

XX P-PSDB; AAB19160.

XX Novel nucleic acid encoding cullin regulating ring finger proteins,
XX termed as ROC proteins similar to anaphase-promoting complex 11, for
XX therapeutic and diagnostic use.

PS Claim 1; Fig 2A; 83pp; English.

PR 18-OCT-2002; 2002US-0418988P.
XX (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX Wu TD, Zhou Y;
XX WPI; 2004-534300/51.
XX
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
XX Claim 1; SEQ ID NO 4374; 5504pp; English.
XX
XX The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

Query Match 100.0%; Score 327; DB 12; Length 506;
Best Local Similarity 100.0%; Pred. No. 2.6e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGCGAGTGGATGGATACCCGAGCGGACCAACAGCGCGGGGCAAGAAG 60
Db 6 ATGGCGGCGAGTGGATGGATACCCGAGCGGACCAACAGCGCGGGGCAAGAAG 65
Qy 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 66 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 125
Qy 121 AACTGTGCCATCTGCAGGACCAATATGATCTTTGATAGTATGATGATGATGATGATGAT 180
Db 126 AACTGTGCCATCTGCAGGACCAATATGATCTTTGATAGTATGATGATGATGATGATGAT 185
Qy 181 GCGTCCGCTACTTTCAGAAAGAGTGTACTGTGCGATGGGGGAGTCTGTAAACCATGCTTTTCAC 240

Db 186 GCGTCCGCTACTTTCAGAAAGAGTGTACTGTGCGATGGGGAGTCTGTAAACCATGCTTTTCAC 245
Qy 241 TTCACATGCGATCTCTCGCTGCTCAAAACAGCAGCAGGTGTGTCCATTGGGACACAGAGAG 300
Db 246 TTCACATGCGATCTCTCGCTGCTCAAAACAGCAGCAGGTGTGTCCATTGGGACACAGAGAG 305
Qy 301 TGGGAATTCCTCAAAAGATATGGCACTAG 327
Db 306 TGGGAATTCCTCAAAAGATATGGCACTAG 332
RESULT 4
ADQ87156
ID ADQ87156 standard; cDNA; 506 BP.
XX
XX AC ADQ87156;
XX
XX DT 07-OCT-2004 (first entry)
XX Human tumour-associated antigenic target (TAT) cDNA sequence #4032.
XX
XX DE Human tumour-associated antigenic target (TAT) cDNA sequence #4032.
XX
XX KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN W02004060270-A2.
XX
XX PD 22-JUL-2004.
XX
XX PF 15-OCT-2003; 2003WO-US029126.
XX
XX PR 18-OCT-2002; 2002US-0418988P.
XX
XX (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
XX Wu TD, Zhou Y;
XX
XX WPI; 2004-534300/51.
XX
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
PS Claim 1; SEQ ID NO 4032; 5504pp; English.
CC
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising

CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT nucleic acid of the invention

SQ Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;

Query Match 100.0%; Score 327; DB 13; Length 508;

Best Local Similarity 100.0%; Pred. No. 2.6e-157;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGTGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60

DB 7 ATGGCGGCGAGTGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 66

QY 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGAT 120

DB 67 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGAT 126

QY 121 AACTGTGCCATCTGCAGGACCAACATATATGGATCTTTTGATAGAAATGTCAAGTAAACCAAG 180

DB 127 AACTGTGCCATCTGCAGGACCAACATATATGGATCTTTTGATAGAAATGTCAAGTAAACCAAG 186

QY 181 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240

DB 187 GCGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 246

QY 241 TTCCACTGCAATCTCGCTGGCTCAAAACACGACAGTGTGTCATTTGGACAAACAGAGAG 300

DB 247 TTCCACTGCAATCTCGCTGGCTCAAAACACGACAGTGTGTCATTTGGACAAACAGAGAG 306

QY 301 TGGGAATTCCAAAGTATGGGCACCTAG 327

DB 307 TGGGAATTCCAAAGTATGGGCACCTAG 333

QY 301 TGGGAATTCCAAAGTATGGGCACCTAG 327

DB 307 TGGGAATTCCAAAGTATGGGCACCTAG 333

QY 301 TGGGAATTCCAAAGTATGGGCACCTAG 327

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QY 301 TGGGAATTCCAAAGTATGGGCACCTAG 327

DB 307 TGGGAATTCCAAAGTATGGGCACCTAG 333

QY 301 TGGGAATTCCAAAGTATGGGCACCTAG 327

DB 307 TGGGAATTCCAAAGTATGGGCACCTAG 333

PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.

XX Claim 1; SEQ ID NO 17191; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030073623

XX Sequence 476 BP; 119 A; 111 C; 124 G; 118 T; 0 U; 4 Other;

Query Match 99.4%; Score 325; DB 9; Length 476;

Best Local Similarity 100.0%; Pred. No. 2.7e-156;

Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCGGCGAGCATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAGCG 62

DB 74 GGCGGCGAGCATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAGCG 133

QY 63 CTTTGAAGTGAAAAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATAA 122

DB 134 CTTTGAAGTGAAAAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATAA 193

QY 123 CTGTGCCATCTGCAGGACCAACATATGGATCTTTGCATAGATGTCACGTCACCAAGCG 182

DB 194 CTGTGCCATCTGCAGGACCAACATATGGATCTTTGCATAGATGTCACGTCACCAAGCG 253

QY 183 GTCCGCTACTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTT 242

DB 254 GTCCGCTACTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTT 313

QY 243 CCACCTGATCTCTCGCTGGCTCAAAAACAGACAGGTGTGTCCATTGGACAAACAGAGAGTG 302

DB 314 CCACCTGATCTCTCGCTGGCTCAAAAACAGACAGGTGTGTCCATTGGACAAACAGAGAGTG 373

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

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QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

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QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

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QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

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QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

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QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

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QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

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QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

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QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

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DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

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QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

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QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

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QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTCCAAAGTATGGGCACCTAG 398

QY 303 GGAATTCCAAAGTATGGGCACCTAG 327

DB 374 GGAATTC

```
XX OS Homo sapiens.
XX PN WO2004080148-A2.
XX PD 23-SEP-2004.
XX PF 30-SEP-2003; 2003WO-US030720.
XX PR 02-OCT-2002; 2002US-0416186P.
XX PA (NUVE-) NOVELO INC.
XX PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
XX PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX DR WPI; 2004-668857/65.
XX DR P-PSDB; ADS10597.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
XX PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX PT aplastic anemia or cancer for promoting wound healing.
XX PS Claim 1; SEQ ID NO 150; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
XX CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX CC be useful in preparing a composition for diagnosing or treating
XX CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX CC disorders, such as aplastic anaemia or cancer, as well as for promoting
XX CC wound healing. The molecules may also be utilised during gene therapy
XX CC procedures. The current sequence is that of a human therapeutic DNA of
XX CC the invention. The current sequence is not shown explicitly within the
XX CC specification but can be accessed from the WIPO web-site.
XX
XX SQ Sequence 3726 BP; 996 A; 955 C; 845 G; 930 T; 0 U; 0 Other;
Query Match 98.2%; Score 321; DB 13; Length 3726;
Best Local Similarity 100.0%; Pred. No. 2.9e-154;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 66
DB 492 GCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 433
QY 67 GAAGTGAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTTGGTTGATACTGT 126
DB 432 GAAGTGAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTTGGTTGATACTGT 373
QY 127 GCCATCTGCAGGAACCAACATTTAGATCTTTGCATAGAATGTCAAGCTAACCGGCTCC 186
DB 372 GCCATCTGCAGGAACCAACATTTAGATCTTTGCATAGAATGTCAAGCTAACCGGCTCC 313
QY 187 GCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 246
DB 312 GCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 253
QY 247 TGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTTGGACAAACAGAGTGGGAA 306
DB 252 TGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTTGGACAAACAGAGTGGGAA 193
QY 307 TTCCAAAGTATGGGCACTAG 327
DB 192 TTCCAAAGTATGGGCACTAG 172
RESULT 10
ACN90161/c
ID ACN90161 standard; DNA; 4543 BP.
XX AC
XX ACN90161;
```

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DT 02-DEC-2004 (first entry)
XX DE Breast cancer related marker, seq id 11311.
XX KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX OS Homo sapiens.
XX PN US2003099974-A1.
XX PD 29-MAY-2003.
XX PF 18-JUL-2002; 2002US-00198846.
XX PR 18-JUL-2001; 2001US-0306220P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX PI WPI; 2003-787014/74.
XX DR Novel isolated polypeptide associated with breast cancer, useful for
XX PT detecting presence of polypeptide in sample, as a marker for breast
XX PT cancer.
XX PS Disclosure; SEQ ID NO 11311; 36pp; English.
XX
XX The invention relates to an isolated polypeptide (I) associated with a
XX CC breast cancer which is encoded by a nucleic acid molecule comprising a
XX CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
XX CC the polypeptide of the invention. The activity of the polypeptide of the
XX CC invention may be described as cytostatic. The antibody is useful for
XX CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
XX CC invention are useful in the detection of breast tumours. (I) is useful as
XX CC a marker for breast cancer and in breast cancer therapy. Sequences given
XX CC in records ACN78851-ACN92934 represent nucleic acid markers associated
XX CC with breast cancer. Note: The sequence listing does not form part of the
XX CC specification but may be obtained in electronic format from the USPTO web
XX CC site at seqdata.uspto.gov/sequence.html?DocID=2003099974
XX
XX SQ Sequence 4543 BP; 1069 A; 1171 C; 1083 G; 1220 T; 0 U; 0 Other;
Query Match 98.2%; Score 321; DB 11; Length 4543;
Best Local Similarity 100.0%; Pred. No. 2.9e-154;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 66
DB 1085 GCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 1026
QY 67 GAAGTGAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTTGGTTGATACTGT 126
DB 1025 GAAGTGAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTTGGTTGATACTGT 966
QY 127 GCCATCTGCAGGAACCAACATTTAGATCTTTGCATAGAATGTCAAGCTAACCGGCTCC 186
DB 965 GCCATCTGCAGGAACCAACATTTAGATCTTTGCATAGAATGTCAAGCTAACCGGCTCC 906
QY 187 GCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 246
DB 905 GCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 846
QY 247 TGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTTGGACAAACAGAGTGGGAA 306
DB 845 TGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTTGGACAAACAGAGTGGGAA 785
QY 307 TTCCAAAGTATGGGCACTAG 327
DB 785 TTCCAAAGTATGGGCACTAG 765
RESULT 11
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ADQ92179
ID ADQ92179 standard; DNA; 503 BP.
XX
AC ADQ92179;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human autoantigen DNA fragment MPMQp800L05536.
XX
ds; autoantigen; antibody; hybridoma; biosensor chip;
KW extracorporeal differential diagnosis; autoimmune disease;
KW ribosomal protein; tubulin;
KW dolichyl-diphospho-oligosaccharide-glycosyl transferase;
KW multiple sclerosis; rheumatoid arthritis; epitope mapping;
KW affinity chromatography; electrophoresis; autoantibody apheresis;
KW RNA interference; RNAi.
XX
XX Homo sapiens.
OS
XX WO2004058972-A1.
PN
XX 15-JUL-2004.
PD
XX 23-DEC-2002; 2002WO-BP014731.
PF
XX 23-DEC-2002; 2002WO-BP014731.
PR
XX (THIE/) THIESEN H.
PA (LORE/) LORENZ P.
PA
XX Thiesen H, Lorenz P;
PI
XX WPI; 2004-543459/52.
DR
XX New human DNA autoantigens, useful as assay, diagnostic, and prognostic
PT reagents and for treating autoimmune disease, also related expression
PT products and antibodies with similar uses.
XX
XX Claim 1; SEQ ID NO 160; 110pp; German.
XX
XX This invention describes novel human DNA autoantigens which are used to
CC produce recombinant expression vectors; prokaryotic or eukaryotic cells;
CC poly- or mono-clonal antibodies (Ab) specific; hybridomas that express
CC monoclonal Ab; biosensor chips having an addressable sequence pattern as
CC probes; medical or diagnostic instruments that include the biosensor; for
CC extracorporeal differential diagnosis of autoimmune diseases and
CC predisposition to them. The autoantigen polynucleotides encode ribosomal
CC proteins; tubulins; dolichyl-diphospho-oligosaccharide-glycosyl
CC transferases and proteins. The antibodies may be labelled conventionally
CC with radioisotopes, coloured or fluorescent groups, or a member of the
CC biotin/avidin pair, or colloidal gold. The autoantigens can be directed
CC against mitochondria, liver-kidney microsomes; histidyl-tRNA; nuclear
CC membrane; neutrophilin/cytoplasm; insect cells; epidermal intracellular
CC or basal membrane antigens; Golgi or cell nuclei, or associated with
CC multiple sclerosis or rheumatoid arthritis. They are useful for epitope
CC mapping; in affinity chromatography or electrophoresis; for diagnosis,
CC prognosis, control of treatment or therapeutic response of autoimmune
CC diseases, particularly in vitro differential diagnosis of autoimmune
CC diseases; to produce biosensor chips or for autoantibody apheresis.
CC Autoantigen DNA can be used for therapeutic RNA interference against
CC autoantibodies. Biochips that carry the new materials are useful in
CC medical and diagnostic instruments. ADQ92020-ADQ92280 represent human
XX autoantigens.
XX
SQ Sequence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other;
Query Match 97.9%; Score 320; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1e-153;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTGG 67
DB 1 CAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTGG 60

QY 68 AAGTGAAGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATGTGTTGATAACTGTG 127
DB 61 AAGTGAAGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATGTGTTGATAACTGTG 120
QY 128 CCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACACGGCGTCCG 187
DB 121 CCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACACGGCGTCCG 180
QY 188 CTACTTCAGAAGAGTGTACTGTGCGATGGGGAGTCTGTAAACCATGCTTTTCACTTCCACT 247
DB 181 CTACTTCAGAAGAGTGTACTGTGCGATGGGGAGTCTGTAAACCATGCTTTTCACTTCCACT 240
QY 248 GCATCTCTCGCTGGCTCAAAAACACGACAGTGTGTCCATTGGACAAACAGAGAGTGGGAAT 307
DB 241 GCATCTCTCGCTGGCTCAAAAACACGACAGTGTGTCCATTGGACAAACAGAGAGTGGGAAT 300
QY 308 TCCAAAAGTATGGGCACTAG 327
DB 301 TCCAAAAGTATGGGCACTAG 320
RESULT 12
ABV25615/C
ID ABV25615 standard; cDNA; 4476 BP.
XX
AC ABV25615;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 25606.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200160860-A2.
PN
XX 23-AUG-2001.
PD
XX 20-FEB-2001; 2001WO-US005171.
PF
XX 17-FEB-2000; 2000US-0183119P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Schlegel R, Endege WO, Monahan JE;
PI
XX WPI; 2001-662795/76.
DR
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 5119-5120; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient

CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX Sequence 4476 BP; 1085 A; 1129 C; 1015 G; 1247 T; 0 U; 0 Other;
 SQ Query Match 94.2%; Score 308; DB 5; Length 4476;
 Best Local Similarity 100.0%; Pred. No. 1.4e-147;
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCAGCGATGATGGATACCCGAGCGGACCAACAGCGCGGGGCAAGAGCGCTTT 66
 DB 1014 GCAGCGATGATGGATACCCGAGCGGACCAACAGCGCGGGGCAAGAGCGCTTT 955

QY 67 GAAGTGAAGTGAATGCAATGAGTCTTGGCGCTGGGATATGTTGGTTGATAACTGT 126
 DB 954 GAAGTGAAGTGAATGCAATGAGTCTTGGCGCTGGGATATGTTGGTTGATAACTGT 895

QY 127 GCCATCTGCAGGACCAATATGATCTTTGCAATAGAAATGCAATACCAAGCGCTCC 186
 DB 894 GCCATCTGCAGGACCAATATGATCTTTGCAATAGAAATGCAATACCAAGCGCTCC 835

QY 187 GCTACTTCAAGAGTGTACTGTGCGATGGGAGTCTGTAACCAATGCTTTTCACTTCCAC 246
 DB 834 GCTACTTCAAGAGTGTACTGTGCGATGGGAGTCTGTAACCAATGCTTTTCACTTCCAC 775

QY 247 TGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACACAGAGTGGAA 306
 DB 774 TGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACACAGAGTGGAA 715

QY 307 TTCGAAAA 314
 DB 714 TTCGAAAA 707

RESULT 13
 ACUS7420
 ID ACUS7420 standard; cDNA; 311 BP.
 XX ACUS7420;
 XX ACUS7420;
 XX 24-MAR-2005 (first entry)
 XX Human colon cancer differentially expressed polynucleotide, SEQ ID:3555.
 DE Differential expression; diagnosis; therapy; drug screening; cancer;
 KW neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;
 KW ss.
 XX Homo sapiens.
 XX WO200500087-A2.
 XX 06-JAN-2005.
 XX 13-MAY-2004; 2004WO-US015421.
 XX 03-JUN-2003; 2003US-0475872P.
 XX (CHIR) CHIRON CORP.
 XX Randazzo F, Moler E, Escobedo J, Garcia PD;
 XX WPI; 2005-075421/08.
 XX New isolated polynucleotides, which are differentially expressed in colon
 PT cancer cell, useful for treating cancer, e.g. colon cancer, breast
 PT cancer, or pancreatic cancer.
 XX
 XX Claim 1; SEQ ID NO 3555; 97pp; English.
 XX The invention relates to 9672 polynucleotides (ACUS3866-ACUS3537) which
 CC are differentially expressed in colon cancer cells. The invention also
 CC relates to vectors and host cells comprising a differentially expressed
 CC polynucleotide of the invention; a method for detecting a cancerous cell

CC by detection of a gene product of the polynucleotides; a method for
 CC inhibiting a cancerous phenotype of a cell by inhibiting a gene product
 CC of the polynucleotides; a method of treating an individual with cancer by
 CC administration of a modulator of a gene product of the polynucleotides;
 CC and an isolated antibody that specifically binds to a polypeptide encoded
 CC by one of the 9672 polynucleotides. The polynucleotides, polypeptides,
 CC antibodies, and methods are useful for the detection of cancerous cells;
 CC for the diagnosis, prognosis and management of cancer; for the
 CC identification of agents that modulate the phenotype of cancerous cells;
 CC for the identification of therapeutic targets for cancer chemotherapy;
 CC and for the treatment of cancer, especially colon cancer and metastasized
 CC colon cancer, but also breast or pancreatic cancer. The polynucleotides
 CC are also useful as a source of probes or primers for use in diagnostic
 CC methods. The differentially expressed polynucleotides or their encoded
 CC proteins can additionally be used as vaccines to modulate primary immune
 CC responses for the prevention or treatment of cancer. The present sequence
 CC represents a specifically claimed polynucleotide which is differentially
 CC expressed in colon cancer. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 311 BP; 77 A; 75 C; 87 G; 72 T; 0 U; 0 Other;

Query Match 90.5%; Score 296; DB 14; Length 311;
 Best Local Similarity 100.0%; Pred. No. 2.1e-141;
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGGCGAGCGATGGATGGATACCCGAGCGGACCAACAGCGCGGGGCAAGAG 60
 DB 16 ATGCGGCGAGCGATGGATGGATACCCGAGCGGACCAACAGCGCGGGGCAAGAG 75

QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
 DB 76 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 135

QY 121 AACTGTGCCATCTGCGAGGACCAACATTTATGGATCTTTGTCATAGAAATGCTCAAGCTAACACAG 180
 DB 136 AACTGTGCCATCTGCGAGGACCAACATTTATGGATCTTTGTCATAGAAATGCTCAAGCTAACACAG 195

QY 181 GCCTCGCTTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC 240
 DB 196 GCCTCGCTTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC 255

QY 241 TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACACACAG 296
 DB 256 TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACACACAG 311

RESULT 14
 ADF42703/c
 ID ADF42703 standard; cDNA; 3484 BP.
 XX ADF42703;
 XX ADF42703;
 XX 26-FEB-2004 (first entry)
 XX Human Testican-1 nucleotide sequence SEQ ID NO:9.
 XX diabetic; pre-diabetic; Type 2 diabetes; antidiabetic; gene therapy;
 KW diabetes; insulin resistance; metabolic disease; human; gene; ss.
 XX Homo sapiens.
 XX WO2003102163-A2.
 XX 11-DEC-2003.
 XX 04-JUN-2003; 2003WO-US017825.
 XX 04-JUN-2002; 2002US-0385857P.
 XX 04-JUN-2002; 2002US-0386013P.
 XX 04-JUN-2002; 2002US-0386074P.

PR 04-JUN-2002; 2002US-0386107P.
PR 05-JUN-2002; 2002US-0386314P.
PR 05-JUN-2002; 2002US-0386326P.
PR 05-JUN-2002; 2002US-0386332P.
PR 05-JUN-2002; 2002US-0386481P.
PR 05-JUN-2002; 2002US-0386512P.
PR 05-JUN-2002; 2002US-0386513P.
PR 05-JUN-2002; 2002US-0386558P.
PR 05-JUN-2002; 2002US-0386600P.
PR 05-JUN-2002; 2002US-0386615P.
PR 05-JUN-2002; 2002US-0386654P.
PR 06-JUN-2002; 2002US-0386838P.
PR 06-JUN-2002; 2002US-0386861P.
PR 06-JUN-2002; 2002US-0386944P.
PR 06-JUN-2002; 2002US-0386955P.
PR 06-JUN-2002; 2002US-0387017P.
PR 06-JUN-2002; 2002US-0387026P.
PR 06-JUN-2002; 2002US-0387039P.
PR 20-JUN-2002; 2002US-0386865P.
XX
PA (META-) METABOLEX INC.
XX
XX Allan B, Gregoire F, Lavan B, Moodie S, Waters S, Wong C;
XX
XX WPI; 2004-053469/05.
DR P-PSDB; ADF42704.
XX
XX Identifying an agent for treating diabetic or pre-diabetic individuals
PT comprises contacting an agent with a polypeptide, e.g., human ceramidase,
PT and selecting an agent that modulates the expression or activity of the
PT polypeptide.
XX
XX Disclosure; SEQ ID NO 9; 209pp; English.
XX
XX The present invention describes a method for identifying an agent for
CC treating a diabetic or pre-diabetic individual. The method comprises
CC contacting an agent to a mixture comprising a polypeptide encoded by a
CC nucleic acid that hybridises under stringent conditions to a nucleic acid
CC encoding any of the 23 fully defined amino acid sequences given in the
CC specification, and selecting an agent that modulates the expression or
CC activity of the polypeptide. Also described: (1) a method of treating a
CC diabetic or pre-diabetic animal, comprising administering to the animal a
CC therapeutic amount of an agent identified by the method described above;
CC (2) a method of introducing an expression cassette into a cell,
CC comprising introducing into the cell an expression cassette comprising a
CC promoter operably linked to a polynucleotide encoding a polypeptide,
CC where the polynucleotide hybridises under stringent conditions to a
CC nucleic acid encoding the above amino acid sequences; and (3) a method of
CC diagnosing an individual who has Type 2 diabetes or is pre-diabetic,
CC comprising detecting in a sample from the individual the level of a
CC polypeptide or the level of the above-mentioned polynucleotide encoding
CC the polypeptide, where a modulated level of the polypeptide or
CC polynucleotide in the sample compared to a level of the polypeptide or
CC polynucleotide in either a lean individual or a previous sample from the
CC individual indicates that the individual is diabetic or pre-diabetic. The
CC method is useful in diagnosing and treating diabetes, insulin resistance
CC or related metabolic diseases in human subjects. The method may also be
CC used in identifying agents for treating diabetic or pre-diabetic
CC individuals. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 3484 BP; 894 A; 910 C; 808 G; 872 T; 0 U; 0 Other;
Query Match 90.5%; Score 296; DB 12; Length 3484;
Best Local Similarity 100.0%; Pred. No. 2e-141;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 66
Db 296 GCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 237
QY 67 GAAGTGAAGAGTGAATGAGTAGCCCTCTGGGCTGGGATATTGGTTGATAACTGT 126

Db 236 GAAGTGAAGAGTGAATGAGTAGCCCTCTGGGCTGGGATATTGGTTGATAACTGT 177
QY 127 GCATCTGCAGGAACCAACATTTATGATCTTTTGCATAGATGTCAAGCTAACGAGCGTCC 186
Db 176 GCATCTGCAGGAACCAACATTTATGATCTTTTGCATAGATGTCAAGCTAACGAGCGTCC 117
QY 187 GCTACTTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATCTTTTCACTTCCAC 246
Db 116 GCTACTTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATCTTTTCACTTCCAC 57
QY 247 TGCATCTCTCGCTGGCTCAAAACACGACAGAGTGTGTCCATTGGACAACAGAGAGTG 302
Db 56 TGCATCTCTCGCTGGCTCAAAACACGACAGAGTGTGTCCATTGGACAACAGAGAGTG 1
RESULT 15
ADQ18564/c
ID ADQ18564 standard; DNA; 3484 BP.
XX
XX AC ADQ18564;
XX
XX 26-AUG-2004 (first entry)
XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 1383.
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
XX ds.
XX Homo sapiens.
XX
XX PN WO2004048938-A2.
XX
XX PD 10-JUN-2004.
XX
XX PF 26-NOV-2003; 2003WO-US038193.
XX
XX PR 26-NOV-2002; 2002US-0429739P.
XX
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX
XX PI Aziz N, Ginsburg WM, Zlotnik A;
XX WPI; 2004-441208/41.
DR
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
XX Example 2; SEQ ID NO 1383; 210pp; English.
XX
XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual,
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 3484 BP; 894 A; 910 C; 808 G; 872 T; 0 U; 0 Other;
Query Match 90.5%; Score 296; DB 12; Length 3484;
Best Local Similarity 100.0%; Pred. No. 2e-141;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 66

Db 296 GCACGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGACGCTTT 237
Qy 67 GAAGTGA AAAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGTTGATAACTGT 126
Db 236 GAAGTGA AAAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGTTGATAACTGT 177
Qy 127 GCCATCTGCAGGAACCAACATTTATCGATCTTTTGCATAGAATGTCAAGCTAACCCAGCGCTCC 186
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Search completed: March 8, 2006, 16:12:25
Job time : 372.547 secs

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GenCore version 5.1.7
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Run on: March 15, 2006, 10:20:40 ; Search time 2414 Seconds
(without alignments)
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Scoring table: OLIGO NUC
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Searched: 5883141 seqs, 28421725653 residues

Word size: 12

Total number of hits satisfying chosen parameters: 435671

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	327	100.0	433	6 CQ698451	Sequence
3	327	100.0	453	6 CQ690099	Sequence
4	327	100.0	467	6 CQ695007	Sequence
5	327	100.0	471	6 CQ712328	Sequence
6	327	100.0	472	6 CQ711142	Sequence
7	327	100.0	482	6 BD027641	Sequence
8	327	100.0	482	6 AX888031	Sequence
9	327	100.0	507	6 CQ729899	Sequence
10	327	100.0	508	6 BD271520	VonHippel
11	327	100.0	508	6 AR640603	Sequence
12	327	100.0	508	6 AF140598	Homo sapi
13	327	100.0	523	6 CQ701366	Sequence
14	327	100.0	535	8 BC001466	Homo sapi
15	327	100.0	535	8 CR456560	Homo sapi
16	327	100.0	554	8 BC017370	Homo sapi
17	320	97.9	503	6 CQ832496	Sequence
18	308	94.2	497	8 HUMYQ60A05	Homo sapi

C	19	308	94.2	4476	6	CQ493737	Sequence
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C	23	267	81.7	5347	6	AX281690	Sequence
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	25	249	76.1	3208	6	AR542209	Sequence
	26	249	76.1	3208	6	AR651451	Sequence
	27	249	76.1	3208	6	AX212267	Sequence
	28	207	63.3	430	6	CQ709825	Sequence
	29	198	60.6	475	6	CQ705678	Sequence
	30	173	52.9	300	6	CQ703590	Sequence
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	39	141	43.1	450	6	CQ686479	Sequence
	40	132	40.4	135	6	CQ668705	Sequence
	41	124	37.9	325	6	CQ708874	Sequence
	42	99	30.3	363	6	CQ688757	Sequence
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ALIGNMENTS

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LOCUS Homo sapiens RING finger protein (ROCI) mRNA, complete cds.
DEFINITION AF142059
ACCESSION AF142059
VERSION AF142059.1 GI:4809215
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 327)
Ohta,T., Michel,J.J., Schottelius,A.J. and Xiong,Y.
AUTHORS ROCI, a homolog of APC11, represents a family of cullin partners with an associated ubiquitin ligase activity
TITLE Mol. Cell 3 (4), 535-541 (1999)
JOURNAL PUBLISHED 10230407
REFERENCE 2 (bases 1 to 327)
Ohta,T., Michel,J.J. and Xiong,Y.
AUTHORS Direct Submission
TITLE Submitted (10-APR-1999) Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Mason Farm Rd. and Manning Dr., Chapel Hill, NC 27599-7295, USA
JOURNAL Location/Qualifiers

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DEFINITION	Sequence 56068 from Patent WO02070737.	linear	PAT 03-FEB-2000
ACCESSION	CO711142		
VERSION	CO711142.1	GI:42271999	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE	1.		
AUTHORS	Liew, C.C., Marshall, W.E. and Zhang, H.		
TITLE	Compositions and methods relating to osteoarthritis		
JOURNAL	Patent: WO 02070737-A 56068 12-SEP-2002;		
	Chondrogene Inc. (CA)		
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Qy	61	CGCTTTGAAGTGA AAAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT	120
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QY 301 TGGGAATTCCAAAGTATGGCACTAG 327
Db 307 TGGGAATTCCAAAGTATGGCACTAG 333
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LOCUS Homo sapiens ring-box protein 1 (RBX1) mRNA, complete cds.
DEFINITION AF140598.1 GI:4769003
ACCESSION Homo sapiens (human)
VERSION 1
KEYWORDS ORGANISM
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS Kamura,T., Koepf,D.M., Conrad,M.N., Skowrya,D., Moreland,R.J.,
Iliopoulos,O., Lane,W.S., Kaelin,W.G. Jr., Elledge,S.J.,
Conaway,R.C., Harper,J.W., and Conaway,J.W.
TITLE Rbx1, a component of the VHL tumor suppressor complex and SCF
ubiquitin ligase
JOURNAL Science 284 (5414), 657-661 (1999)
PUBMED 10213691
REFERENCE 2 (bases 1 to 508)
AUTHORS Kamura,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma
Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA
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Db 307 TGGGAATTCCAAAGTATGGCACTAG 333
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LOCUS Homo sapiens
DEFINITION Sequence 46292 from Patent WO02070737.
ACCESSION CO701366
VERSION 1
KEYWORDS CO701366.1 GI:42262133
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 46292 12-SEP-2002;
Chondrogene Inc. (CA)
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REFERENCE 2 (bases 1 to 535)
 AUTHORS Collins,J.E., Wright,C.L., Edwards,C.A., Davis,M.P., Grinham,J.A., Cole,C.G., Goward,M.E., Aguado,B., Mallya,M., Mokrab,Y., Huckle,E.J., Beare,D.M. and Dunham,I.
 TITLE Direct Submission
 JOURNAL Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: c22g@sanger.ac.uk Manuscript
 COMMENT Sanger Institute name : pGEM.RBX1
 Homo sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see http://www.sanger.ac.uk/HGP/Chr22/.

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 DEFINITION
 ACCESSION BC017370
 VERSION BC017370.1 GI:169924201
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 554)
 REFERENCE
 AUTHORS Klausner,R.D., Feingold,E.A., Grouse,L.H., Derge,J.G., Strausberg,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,I., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Ussin,T.B., Toshiyuki,S., Carininci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., C., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 2 (bases 1 to 554)
 REFERENCE
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (13-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
 http://www.systemsbio.org
 contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Series: IRAL Plate: 19 Row: c Column: 17
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22091459.
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DB	1 TGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTGAAGTGAAAAAGT 60
QY	80 GGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATACTGTGCCATCTGCAGGA 139
DB	61 GGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATACTGTGCCATCTGCAGGA 120
QY	140 ACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCGGGCTCGCTTCTCAGAAG 199
DB	121 ACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCGGGCTCGCTTCTCAGAAG 180
QY	200 AGTGTAAGTCGATGGGAGTCTGTAACCATGCTTTTCACTTCCACTGATCTCTCGCT 259
DB	181 AGTGTAAGTCGATGGGAGTCTGTAACCATGCTTTTCACTTCCACTGATCTCTCGCT 240
QY	260 GGCTCAAAACACGACAGTGTGTCATTGGACAACAGAGAGTGGAAATTCAAAAGTATG 319
DB	241 GGCTCAAAACACGACAGTGTGTCATTGGACAACAGAGAGTGGAAATTCAAAAGTATG 300
QY	320 GGCACCTAG 327
DB	301 GGCACCTAG 308
RESULT 19	
CQ493737/c	
LOCUS	
Sequence 25604 from Patent WO0160860.	
ACCESSION	
CQ493737	
VERSION	
CQ493737.1 GI:41459356	
KEYWORDS	
Homo sapiens (human)	
SOURCE	
ORGANISM	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
Hominidae; Homo.	
REFERENCE	
1	
Schlegel R., Endege W.O. and Monahan J.E.	
Genes differentially expressed in human prostate cancer and their	
use	
Patent: WO 0160860-A 25604 23-AUG-2001;	
JOURNAL	
The location of this clone is unknown.	
FEATURES source	Location/Qualifiers
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	/db_xref="taxon:9606"
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3. .305	
/note="similar to Caenorhabditis elegans protein Z70757 (PID:g1262999)"	
misc_feature	
18. .284	
/note="similar to Caenorhabditis elegans protein U80449 (PID:g1707068)"	
misc_feature	
36. .302	
/note="similar to Saccharomyces cerevisiae protein S66830 (PID:g2132017)"	
misc_feature	
42. .302	
/note="similar to Schizosaccharomyces pombe protein Z98977 (PID:g2388937)"	
misc_feature	
51. .284	
/note="similar to Caenorhabditis elegans protein Z46242 (PID:g559430)"	
ORIGIN	
Query Match 94.2%; Score 308; DB 8; Length 497;	
Best Local Similarity 100.0%; Pred. No. 9.1e-173;	
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	20 TGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTGAAGTGAAAAAGT 79
DB	1 TGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTGAAGTGAAAAAGT 60
QY	80 GGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATACTGTGCCATCTGCAGGA 139
DB	61 GGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATACTGTGCCATCTGCAGGA 120
QY	140 ACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCGGGCTCGCTTCTCAGAAG 199
DB	121 ACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCGGGCTCGCTTCTCAGAAG 180
QY	200 AGTGTAAGTCGATGGGAGTCTGTAACCATGCTTTTCACTTCCACTGATCTCTCGCT 259
DB	181 AGTGTAAGTCGATGGGAGTCTGTAACCATGCTTTTCACTTCCACTGATCTCTCGCT 240
QY	260 GGCTCAAAACACGACAGTGTGTCATTGGACAACAGAGAGTGGAAATTCAAAAGTATG 319
DB	241 GGCTCAAAACACGACAGTGTGTCATTGGACAACAGAGAGTGGAAATTCAAAAGTATG 300
QY	320 GGCACCTAG 327
DB	301 GGCACCTAG 308
RESULT 19	
CQ493737/c	
LOCUS	
Sequence 25604 from Patent WO0160860.	
ACCESSION	
CQ493737	
VERSION	
CQ493737.1 GI:41459356	
KEYWORDS	
Homo sapiens (human)	
SOURCE	
ORGANISM	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
Hominidae; Homo.	
REFERENCE	
1	
Schlegel R., Endege W.O. and Monahan J.E.	
Genes differentially expressed in human prostate cancer and their	
use	
Patent: WO 0160860-A 25604 23-AUG-2001;	
JOURNAL	
The location of this clone is unknown.	
FEATURES source	Location/Qualifiers
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misc_feature	
94.2%; Score 308; DB 6; Length 4476;	
Best Local Similarity 100.0%; Pred. No. 9.9e-173;	
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
ORIGIN	
Query Match 94.2%; Score 308; DB 6; Length 4476;	
Best Local Similarity 100.0%; Pred. No. 9.9e-173;	
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	7 GCAGCGATGATGCGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 66
DB	1014 GCAGCGATGATGCGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 955
QY	67 GAAGTGAATAAGTGAATGCAATGAGTACCCCTCTGGGCTGGGATATTGTGGTTGATAACTGT 126
DB	954 GAAGTGAATAAGTGAATGCAATGAGTACCCCTCTGGGCTGGGATATTGTGGTTGATAACTGT 895
QY	127 GCCATCTGCAGGAACACCATATTGGATCTTTGCATAGAAATGTCAGGTCACAGGCGTCC 186
DB	894 GCCATCTGCAGGAACACCATATTGGATCTTTGCATAGAAATGTCAGGTCACAGGCGTCC 835
QY	187 GCTACTTCAGAAGAGTGTACTGTGCGATGGGAGTCTGTACCATGCTTTTCACTTCCAC 246
DB	834 GCTACTTCAGAAGAGTGTACTGTGCGATGGGAGTCTGTACCATGCTTTTCACTTCCAC 775
QY	247 TGCATCTCTCGCTGCTCAAAACACGACAGTGTGTCCATTGGACAAACAGAGAGTGGAA 306
DB	774 TGCATCTCTCGCTGCTCAAAACACGACAGTGTGTCCATTGGACAAACAGAGAGTGGAA 715
QY	307 TTCCAAAA 314
DB	714 TTCCAAAA 707
RESULT 20	
HSTEST/c	
LOCUS	
H. sapiens mRNA for testican.	
ACCESSION	
X73608	
VERSION	
X73608.1 GI:793844	
KEYWORDS	
testican.	
SOURCE	
Homo sapiens (human)	
ORGANISM	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
Hominidae; Homo.	
REFERENCE	
1 (bases 1 to 3484)	
Alliel P.M., Perin J.P., Jolles P. and Bonnet F.J.	
Testican, a multidomain testicular proteoglycan resembling	
modulators of cell social behaviour	
Eur. J. Biochem. 214 (1), 347-350 (1993)	
JOURNAL	
PUBMED	
8389704	
FEATURES	
source	
1. .3484	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone_lib="lambda gt11"	
435. .1754	
/codon_start=1	
/product="testican"	
/protein_id="CAA5199.1"	
/db_xref="GI:793845"	
/db_xref="GOA:Q08629"	
/db_xref="InterPro:IPR000716"	
/db_xref="UniProt/Swiss-Prot:Q08629"	
/translation="MPATAVLAAAAACWCFQVESRHLDALAGGAGNHNFLDNQW	
LSTVSQYDRDKYWNRPDDYFRWNPNKPFQDALDPSKDPCLVKVSPKVCVTQDY	
QTALCVSRHLLPQKNGKAGWVGPSNLVCKPCPVAQSAWVCSDGSHYSYKSK	
LEFHACSTGKSLATLCDGCPCLPEPKHKAERSACTDKELRNLAARLQWGA	

EDANRVIKPTSSNTAQGRDFTSILPICKDSLGMWFKLDMNYDLLDPPSEINAIYLDK
YEPCKIPLFNSCDFGDKGLSNNEWCYCFQKPGGLPCQNEMNRIOKLSKGKSLGAFI
PRCNEEYKATQCSGQCWCVDKYNGELAGSRKQACVCEEBOETSGDFTGSGSGSV
VLDDLEYRELPGDKKEGLRVHTRAVTADDEDEDDKEDVSGYTW

VEEDDELEIIEIDTSGE	NQKDGQRNVRHAKAVIIEDDDDDDDAGGDEYGVLIW
ORIGIN	
Query Match	90.5%; Score 296; DB 8; Length 3484;
Best Local Similarity	100.0%; Pred. No. 1.6e-165;
Matches 296; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

Qy	7	GCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGGCCGCGGCAAGACGCGCTTT	66
Db	296	GCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGGCCGCGGCAAGACGCGCTTT	237

Qy 67 GAAGTGA AAAAGTGGGAATGCAGTAGCCCTCTGGGCCCTGGGATAATTGTGGTTGATAACTGT 126

Db 236 GAAGTGA AAAAGTGGGAATGCAGTAGCCCTCTGGGCCCTGGGATAATTGTGGTTGATAACTGT 177

Qy 127 GCCATCTCAGGAACCAATTATGGATCTTTGGCATAGAAATGCTCAAGCTAACCAAGGCGTCC 186

Db 176 GCCATCTCAGGAACCAATTATGGATCTTTGGCATAGAAATGCTCAAGCTAACCAAGGCGTCC 117

Qy	187	GCTACTTCAGAGAGTGTACTGTCGCATGGGGAGTCTGTAAACATGCTTTTCATTCCAC	246
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Db	116	GCTACTTCAGAGAGTGTACTGTCGCATGGGGAGTCTGTAAACATGCTTTTCATTCCAC	57

[illegible]

RESULT 21
NY000760

LOCUS AY099360 Homo sapiens zyp protein mRNA, partial cds.
DEFINITION Homo sapiens zyp protein mRNA, partial cds.
ACCESSION AY099360
VERSION AY099360.1
KEYWORDS

KEYWORDS	SOURCE	ORGANISM
.	Homo sapiens (human)	
.	Homo sapiens	
.	Homo sapiens	

REFERENCE

1 (bases 1 to 306)

Hominidae; Homo.

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

TITLE Rieger, F. and Alliel, P. M.
Genomic organization and expression of the ubiquitin-proteasome complex-associated protein Rbx1/ROC1/Hrt1

PUBMED
10643962
2 (bases 1 to 306)
REFERENCE
Alltel, P.M., Seddiqui, N., Belkadi, L., Lecoœur, L. and Perin, J. P.
AUTHORS

JOURNAL Submitted (23-APR-2002) U488, INSERM, 80, rue du General Leclerc,
Le Kremlin-Bicetre 94270, France
FEATURES Location/Qualifiers

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/mol_type="mrna"  
/db_xref="taxon:9606"
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/sex="male"
/cross="11p"
/tissue_type="whole brain"
/dev_stages="26-week fetus"

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CDS
/notes="similar to REX1/ROCl/HRT1"
/codon start=3
/notes="caucasian"
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/db_xref = "GI: 2052055"
/translation = "NSGASKRPFVKKKNAAVAIWAWDIVVUNCAICRNHTMDICTEQ

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Query Match 84.1%; Score 275; DB 8; Length 306;
 Best Local Similarity 100.0%; Pred. No. 5.7e-153;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	53	16
Db	GCAAGAACGCTTTGAAGTGAAAAAGTGAATGCAGTAGCCCTCTGGGCGTGGGATATTG	112
		75

Qy	113	TGGTTGATAACTGTGCGCATCTGCAGAACCA	CATTATGGATCTCTTTG	CATAGTAATGTC	CAAG	172
Dδ	76	TGGTTGATAACTGTGCGCATCTGCAGAACCA	CATTATGGATCTCTTTG	CATAGTAATGTC	CAAG	135

Qy 173 CTAAACAGCGGTCGCTACTTTCAGAGAGTGTACTCTCGATCGGGAGTCGTAAACCATG 232

Db 136 CTAAACAGCGGTCGCTACTTTCAGAGAGTGTACTCTCGATCGGGAGTCGTAAACCATG 195

Qy	233	CTTTTCACCTTCGATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACA	292
Db	196	CTTTTCACCTTCGATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACA	255

Qy		293	ACAGAGATGGAA	TTCCAAAGTATGGGCTACTAG	327
Dh		256	ACAGAGATGGGA	TTCCAAGTAGTGGGCCTAG	290

RESULT 22
CG702220

LOCUS CQ702730 468 bp DNA
DEFINITION Sequence 47656 from Patent WO02070737.
ACCESSION CQ702730
VERSION CQ702730.1 C1.42262249
FEATURES
ORIGIN 1 CT..42262249
PAT 03-FEB-2000
linear

KEYWORDS
SOURCE
Homo sapiens (human)
Homo sapiens
ORGANISM

REFERENCE

1. J. A. C. Marshall, Mammals of the World, Vol. 1, p. 607. Wm. B. Saunders Co., Philadelphia, Pa., 1932.

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 47656 12-SEP-2002;
Chondrogene Inc. (CA) 3,516,100

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source
1. .468
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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	Matches	270;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	51	GGGCGAAGAAGCGCTTTGAAGTGAAAAAGTGGAAATGCAGTTAGCCCTCTGGGCTGGGATAT	110							

Db	24	GGGCAAGAGCGCCTTTGAAAGTGAAAAAGTGGAAATGCAGTAGCCCTCTGGGCGCTGGGATAT	83
Qy	111	TGTGGTTGATAAAGTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGAAATGTCA	170

Db	84	TGTGGTTGATAACTGTGCCACTCTGACGGAAACCACTTAATGGATCTTTGCATAGAAATGTCA	143
Qv	171	AGCTAACCCAGGCGTCCGCTACTTTCAGAAGAGTGTACTGTGCATGGGGAGTCTGTAAACCA	230

Db	144	AGCTAACCGAGCGTCCGCTACTTCAGAAGAGTGTACTGTCGATCGGGAGTCTGTAAACCA	203
Ov	231	TGCTTTTTCACTTCCACTGCAATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTTGA	290

Db	204	TGCTTTTCACATTCACATGCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATGGA	263
Qv	291	CAACACAGAGTGGGAATTCCAAAGATGG	320

—

RESULT 26
AR651451
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

AB651451
Sequence 27 from patent US 6881563.
AR651451
AR651451.1 GI:62795924
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 3208)
Donoho,G., Scoville,J., Turner,C.A. Jr., Friedrich,G., Abuin,A.,
Zambrowicz,B. and Sands,A.T.
Human proteases and polynucleotides encoding the same
Patent: US 6881563-A 27 19-APR-2005;
Lexicon Genetics Incorporated; The Woodlands, TX
Location/Qualifiers
1..3208
/organism="unknown"
/mol_type="genomic DNA"

Query Match 76.1%; Score 249; DB 6; Length 3208;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TGGNATGACAGTGGCCCTCTGGGCTGGGATATTGTTGATTAATCTGCAATCTGCAGG 138
DB 2776 TGGAAATGACAGTGGCCCTCTGGGCTGGGATATTGTTGATTAATCTGCAATCTGCAGG 2835

QY 139 AACACATTTAGTATCTTTGCATAGAATGCAAGCTAACACAGGCGTCCGCTACTTTCAGAA 198
DB 2836 AACACATTTAGTATCTTTGCATAGAATGCAAGCTAACACAGGCGTCCGCTACTTTCAGAA 2895

QY 199 GAGTGTACTTGCATGGGAGTCTGTAACCATGCTTTTTCACCTTCCACTGCAATCTCTCGC 258
DB 2896 GAGTGTACTTGCATGGGAGTCTGTAACCATGCTTTTTCACCTTCCACTGCAATCTCTCGC 2955

QY 259 TGGCTCAAAACACAGAGGTGTCCATTGGACACAGAGTGGGAATTCCTCAAAAGTAT 318
DB 2956 TGGCTCAAAACACAGAGGTGTCCATTGGACACAGAGTGGGAATTCCTCAAAAGTAT 3015

QY 319 GGGCACTAG 327
DB 3016 GGGCACTAG 3024

RESULT 27
AX212267
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

AX212267
Sequence 27 from Patent W00159134.
AX212267
AX212267.1 GI:15524031
Homo sapiens (human)
Homo sapiens
Homo sapiens
Donoho,G., Scoville,J., Turner,C.A., Friedrich,G.B., Abuin,A.,
Zambrowicz,B. and Sands,A.T.
Human proteases and polynucleotides encoding the same
Patent: W0 0159134-A 27 16-AUG-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
1..3208
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 76.1%; Score 249; DB 6; Length 3208;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2776 TGGAAATGACAGTGGCCCTCTGGGCTGGGATATTGTTGATTAATCTGCAATCTGCAGG 2835

QY 139 AACACATTTAGTATCTTTGCATAGAATGCAAGCTAACACAGGCGTCCGCTACTTTCAGAA 198
DB 2836 AACACATTTAGTATCTTTGCATAGAATGCAAGCTAACACAGGCGTCCGCTACTTTCAGAA 2895

QY 199 GAGTGTACTTGCATGGGAGTCTGTAACCATGCTTTTTCACCTTCCACTGCAATCTCTCGC 258
DB 2896 GAGTGTACTTGCATGGGAGTCTGTAACCATGCTTTTTCACCTTCCACTGCAATCTCTCGC 2955

QY 259 TGGCTCAAAACACAGAGGTGTCCATTGGACACAGAGTGGGAATTCCTCAAAAGTAT 318
DB 2956 TGGCTCAAAACACAGAGGTGTCCATTGGACACAGAGTGGGAATTCCTCAAAAGTAT 3015

QY 319 GGGCACTAG 327
DB 3016 GGGCACTAG 3024

RESULT 28
CQ709825
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

CQ709825
Sequence 54751 from Patent W002070737.
CQ709825
CQ709825.1 GI:42270679
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 54751 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 63.3%; Score 207; DB 6; Length 430;
Best Local Similarity 99.7%; Pred. No. 3.8e-112;
Matches 327; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGCGCGCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
DB 21 ATGCGCGCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 80

QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
DB 81 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 140

QY 121 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTTGCATAGATCTCAAGCTAA-CCA 179
DB 141 AACTGTGCCATCTGCAGGAACCAATTTATGGATCTTTTGCATAGATCTCAAGCTAA-CCA 200

QY 180 GGCCTCCGCTACTTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTTCA 239
DB 201 GGCCTCCGCTACTTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTTCA 260

QY 240 CTTTCCACTGCAATCTCTCGCTGGCTCAAAACACAGAGGTGTGTCCATTGGACACAGAGA 299
DB 261 CTTTCCACTGCAATCTCTCGCTGGCTCAAAACACAGAGGTGTGTCCATTGGACACAGAGA 320

Db	226	TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG	275
RESULT 32			
AX894508			
LOCUS	AX894508	402 bp	DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 10371 from Patent EP1033401.		
ACCESSION	AX894508		
VERSION	AX894508.1	GI:40049392	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.		
TITLE	Expressed sequence tags and encoded human proteins		
JOURNAL	Patent: Ep 1033401-A 10371 06-SEP-2000;		
GENSET (FR)	Genset (FR)		
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Query Match	52.0%;	Score 170;	DB 6; Length 402;
Best Local Similarity	100.0%;	Pred. No. 6.2e-90;	
Matches	170;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	158	GCATAGAAATGCTCAAGCTAACACAGCGTCCGCTACTTCCAGAAGAGTGACTGTGCGCATGGG	217
Db	106	GCATAGAAATGCTCAAGCTAACACAGCGTCCGCTACTTCCAGAAGAGTGACTGTGCGCATGGG	165
Qy	218	GAGTCTGTAAACCATGCTTTTTCACCTCCACTGCGATCTCTCGCTGGCTCAAAACACGACAGG	277
Db	166	GAGTCTGTAAACCATGCTTTTTCACCTCCACTGCGATCTCTCGCTGGCTCAAAACACGACAGG	225
Qy	278	TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG	327
Db	226	TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG	275
RESULT 33			
BD119236			
LOCUS	BD119236	463 bp	DNA linear PAT 18-SEP-2002
DEFINITION	EST and encoded human protein.		
ACCESSION	BD119236		
VERSION	BD119236.1	GI:23214146	
KEYWORDS	JP 2002010789-A/11313.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.		
TITLE	EST and encoded human protein		
JOURNAL	Patent: JP 2002010789-A 11313 15-JAN-2002;		
GENSET CORP	Genset CORP		
COMMENT			
OS	Homo sapiens (human)		
PN	JP 2002010789-A/11313		
PD	15-JAN-2002		
PF	07-AUG-2000	JP 2000280989	
PR	05-AUG-1999	US 60/147499	
PI	JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI		
GIORDANO			
PC	C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC		
C12N1/21,			
PC	C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC		
C12N15/00			
CC	n=a, g, c or t		
PH	Key		
FT	misc		
FEATURES			
source	Location/Qualifiers		
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	/db_xref="taxon:9606"		
ORIGIN			
Query Match	52.0%;	Score 170;	DB 6; Length 463;
Best Local Similarity	100.0%;	Pred. No. 6.3e-90;	
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Qy	158	GCATAGAAATGCTCAAGCTAACACAGCGTCCGCTACTTCCAGAAGAGTGACTGTGCGCATGGG	217
Db	101	GCATAGAAATGCTCAAGCTAACACAGCGTCCGCTACTTCCAGAAGAGTGACTGTGCGCATGGG	160
Qy	218	GAGTCTGTAAACCATGCTTTTTCACCTCCACTGCGATCTCTCGCTGGCTCAAAACACGACAGG	277
Db	161	GAGTCTGTAAACCATGCTTTTTCACCTCCACTGCGATCTCTCGCTGGCTCAAAACACGACAGG	220
Qy	278	TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG	327
Db	221	TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG	270
RESULT 34			
AR423683			
LOCUS	AR423683	463 bp	DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 15180 from patent US 6639063.		
ACCESSION	AR423683		
VERSION	AR423683.1	GI:40178793	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 463)		
AUTHORS	Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.		
TITLE	EST's and encoded human proteins		
JOURNAL	Patent: US 6639063-A 15180 28-OCT-2003;		
GENSET S.A.;;	WOX;		
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Best Local Similarity	100.0%;	Pred. No. 6.3e-90;	
Matches	170;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	158	GCATAGAAATGCTCAAGCTAACACAGCGTCCGCTACTTCCAGAAGAGTGACTGTGCGCATGGG	217
Db	101	GCATAGAAATGCTCAAGCTAACACAGCGTCCGCTACTTCCAGAAGAGTGACTGTGCGCATGGG	160
Qy	218	GAGTCTGTAAACCATGCTTTTTCACCTCCACTGCGATCTCTCGCTGGCTCAAAACACGACAGG	277
Db	161	GAGTCTGTAAACCATGCTTTTTCACCTCCACTGCGATCTCTCGCTGGCTCAAAACACGACAGG	220
Qy	278	TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG	327
Db	221	TGTGTCATTGGACACAGAGTGGGAATTCCAAAGATATGGGCACCTAG	270
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AX984377			
LOCUS	AX984377	463 bp	DNA linear PAT 15-JAN-2004
DEFINITION	Sequence 15180 from Patent EP104808.		
ACCESSION	AX984377		
VERSION	AX984377.1	GI:40990517	
KEYWORDS			

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1
 AUTHORS Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
 TITLE ESTs and encoded human proteins
 JOURNAL Patent: EP 1104808-A 15180 06-JUN-2001;
 Genset (FR)

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 /db_xref="taxon:9606"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 6.3e-90; Mismatches 0; Indels 0; Gaps 0;
 Matches 170; Conservative 0

QY 158 GCATAGAAATGCTCAAGCTAACCGCGCTCCGCTACTTTCAGAGAGTGTACTGTGCGCATGGG 217
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 Db 101 GCATAGAAATGCTCAAGCTAACCGCGCTCCGCTACTTTCAGAGAGTGTACTGTGCGCATGGG 160
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QY 218 GAGTCTGTAAACCATGTTTTCATCTCCACTGCAATCTCTCGCTCGCTCAAAACACGACAGG 277
 |||||
 Db 161 GAGTCTGTAAACCATGTTTTCATCTCCACTGCAATCTCTCGCTCGCTCAAAACACGACAGG 220
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QY 278 TGTGTCATTTGGACACAGAGTGGGAATTCAAAAGTATGGGCCTAG 327
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 Db 221 TGTGTCATTTGGACACAGAGTGGGAATTCAAAAGTATGGGCCTAG 270
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RESULT 36
 CQ674921
 LOCUS 370 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 19847 from Patent WO02070737.
 ACCESSION CQ674921
 VERSION CQ674921.1 GI:42176542
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1
 AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
 TITLE Compositions and methods relating to osteoarthritis
 JOURNAL Patent: WO 02070737-A 19847 12-SEP-2002;
 Chondrogene Inc. (CA)

FEATURES
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
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 Best Local Similarity 99.5%; Pred. No. 9.9e-86; Mismatches 1; Indels 0; Gaps 0;
 Matches 213; Conservative 0

QY 114 GGTGTAACTGTGGCCATCTGCAGAACACCAATTATGGATCTTTTGCATAGAAATGTCAAGC 173
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 Db 3 GGTGTAACTGTGGCCATCTGCAGAACACCAATTATGGATCTTTTGCATAGAAATGTCAAGC 62
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QY 174 TAACACGGCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGGAGTCTGTAAACCATGC 233
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 Db 63 TAACACGGCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGGAGTCTGTAAACCATGC 122
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QY 234 TTTTCACTTCCACTGCAATCTCTCGCTGGCTCAAAACACAGAGTGTGTCATTGGACAA 293
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 Db 123 TTTTCACTTCCACTGCAATCTCTCGCTGGCTCAAAACACAGAGTGTGTCATTGGACAA 182
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QY 294 CAGAGAGTGGGAATTCAAAAGTATGGGCCTAG 327
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 Db 183 CAGAGAGTGGGAATTCAAAAGTATGGGCCTAG 216
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RESULT 37
 CQ680807
 LOCUS 318 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 25733 from Patent WO02070737.
 ACCESSION CQ680807
 VERSION CQ680807.1 GI:42196893
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1
 AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
 TITLE Compositions and methods relating to osteoarthritis
 JOURNAL Patent: WO 02070737-A 25733 12-SEP-2002;
 Chondrogene Inc. (CA)

FEATURES
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

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 Matches 157; Conservative 0

QY 1 ATGGCGGCGAGCATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
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 Db 20 ATGGCGGCGAGCATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
 |||||

QY 61 CGCTTTTGAAGTGAAGTGGGAATGCAATGAGTACCTCTGGGCTGGGATATTTGGTTGAT 120
 |||||
 Db 80 CGCTTTTGAAGTGAAGTGGGAATGCAATGAGTACCTCTGGGCTGGGATATTTGGTTGAT 139
 |||||

QY 121 AACTGTGCCATCTGCAGGACCAACATTTGGATCTTT 157
 |||||
 Db 140 AACTGTGCCATCTGCAGGACCAACATTTGGATCTTT 176
 |||||

RESULT 38
 CQ707821
 LOCUS 486 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 52747 from Patent WO02070737.
 ACCESSION CQ707821
 VERSION CQ707821.1 GI:42268590
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1
 AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
 TITLE Compositions and methods relating to osteoarthritis
 JOURNAL Patent: WO 02070737-A 52747 12-SEP-2002;
 Chondrogene Inc. (CA)

FEATURES
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 1e-76; Mismatches 0

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Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 96 CTGGGCTGGGATATGTTGGTTGATACTGTCATCGCCATCGCAGGACACACATTATGGATCT 155
Db 91 CTGGGCTGGGATATGTTGGTTGATACTGTCATCGCCATCGCAGGACACACATTATGGATCT 150
Qy 156 TTGCATAGAATGTCAAGCTAACCCAGGCGTCCGCTACTTTCAGAAGAGTGTACTGTCCGATG 215
Db 151 TTGCATAGAATGTCAAGCTAACCCAGGCGTCCGCTACTTTCAGAAGAGTGTACTGTCCGATG 210
Qy 216 GGGAGTCTGTAAACCATGCTTTTCACTTC 243
Db 211 GGGAGTCTGTAAACCATGCTTTTCACTTC 238

RESULT 39
LOCUS CO686479 450 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 31405 from Patent WO02070737.
ACCESSION CO686479
VERSION CO686479.1 GI:42215585
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 31405 12-SEP-2002;
Chondrogene Inc. (CA)
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source Location/Qualifiers
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Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 158 GCATAGAATGTCAAGCTAACCCAGGCGTCCGCTACTTTCAGAAGAGTGTACTGTCCGATGG 217
Db 109 GCATAGAATGTCAAGCTAACCCAGGCGTCCGCTACTTTCAGAAGAGTGTACTGTCCGATGG 168
Qy 218 GAGTCTGTAAACCATGCTTTTCACTTCCACTGCATCTCTCGCTGCTCAAAACACGACAGG 277
Db 169 GAGTCTGTAAACCATGCTTTTCACTTCCACTGCATCTCTCGCTGCTCAAAACACGACAGG 228
Qy 278 TGTGTCCATTGGACAACAGAG 298
Db 229 TGTGTCCATTGGACAACAGAG 249

RESULT 40
LOCUS CO688705 135 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 13631 from Patent WO02070737.
ACCESSION CO688705
VERSION CO688705.1 GI:42157083
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 13631 12-SEP-2002;
Chondrogene Inc. (CA)
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FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.9e-67;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGCGGCAGCGATGGATGTGGATACCCCGAGCGCACCAACACGCGCGGCAAGAAG 60
Db 4 ATGGCGGCAGCGATGGATGTGGATACCCCGAGCGCACCAACACGCGCGGCAAGAAG 63
Qy 61 CGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGCGCTGGGATATTGTGTTGAT 120
Db 64 CGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGCGCTGGGATATTGTGTTGAT 123
Qy 121 AACGTGTGCCATC 132
Db 124 AACGTGTGCCATC 135

RESULT 41
LOCUS CO708874 325 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 53800 from Patent WO02070737.
ACCESSION CO708874
VERSION CO708874.1 GI:42269668
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 53800 12-SEP-2002;
Chondrogene Inc. (CA)
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Db 82 GCATAGAATGTCAAGCTAACCCAGGCGTCCGCTACTTTCAGAAGAGTGTACTGTCCGATGG 141
Qy 218 GAGTCTGTAAACCATGCTTTTCACTTCCACTGCATCTCTCGCTGCTCAAAACACGACAGG 277
Db 142 GAGTCTGTAAACCATGCTTTTCACTTCCACTGCATCTCTCGCTGCTCAAAACACGACAGG 201
Qy 278 TGTG 281
Db 202 TGTG 205

RESULT 42
LOCUS CO688757 363 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 33683 from Patent WO02070737.
ACCESSION CO688757
VERSION CO688757.1 GI:42221728
KEYWORDS
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Liew.C.C., Marshall.W.E. and Zhang.H.
AUTHORS Compositions and methods relating to osteoarthritis
TITLE Patent: WO 02070737-A 33683 12-SEP-2002;
JOURNAL Chondrogene Inc. (CA)
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QY 229 CATGCTTTTCACCTCCACTGCATCTCTCGCTGCTCAAAACACGACGAGGTGTGCCATTG 288
Db 93 CATGCTTTTCACCTCCACTGCATCTCTCGCTGCTCAAAACACGACGAGGTGTGCCATTG 152
QY 289 GACACACAGAGTGGGAATTCCTCAAAAGTATGGGCACCTAG 327
Db 153 GACACACAGAGTGGGAATTCCTCAAAAGTATGGGCACCTAG 191
RESULT 43
AK090764
LOCUS Homo sapiens cDNA FLJ33445 fis, clone BRALZ2000263.
DEFINITION AK090764
ACCESSION AK090764.1 GI:21748986
VERSION
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Ota.T., Suzuki.Y., Nishikawa.T., Otsuki.T., Sugiyama.T., Irie.R.,
AUTHORS Wakamatsu.A., Hayaashi.K., Sato.H., Nagai.K., Kimura.K., Makita.H.,
Sekine.M., Obayashi.M., Nishi.T., Shibahara.T., Tanaka.T.,
Ishii.S., Yamamoto.J., Saito.K., Kawai.Y., Isono.Y., Nakamura.Y.,
Nagahari.K., Murakami.K., Yasuda.T., Iwayanagi.T., Wagatsuma.M.,
Shiratori.A., Sudo.H., Hosoiri.T., Kaku.Y., Kodaira.H., Kondo.H.,
Sugawara.M., Takahashi.M., Kanda.K., Yokoi.T., Furuya.T.,
Kikkawa.B., Omura.Y., Abe.K., Kamihara.K., Katsuta.N., Sato.K.,
Tanikawa.M., Yamazaki.M., Ninomiya.K., Ishibashi.T., Yamashita.H.,
Murakawa.K., Fujimori.K., Tanai.H., Kimata.M., Watanabe.M.,
Hiraoka.S., Chiba.Y., Ishida.S., Ono.Y., Takiguchi.S., Watanabe.S.,
Yosida.M., Hotuta.T., Kusano.J., Kanehori.K., Komai.F., Hara.R.,
Hara.H., Tanase.T., Nomura.Y., Togiya.S., Komai.F., Hara.R.,
Takeuchi.K., Arita.M., Imose.N., Musashino.K., Yuuki.H., Oshima.A.,
Sasaki.N., Aotsuka.S., Yoshikawa.Y., Matsunawa.H., Ichihara.T.,
Shiohata.N., Sano.S., Moriya.S., Momiyama.H., Satoh.N., Takami.S.,
Terahima.Y., Suzuki.O., Nakagawa.S., Senoh.A., Mizoguchi.H.,
Goto.Y., Shimizu.F., Wakebe.H., Hiebigaki.H., Watanabe.T.,
Sugiyama.A., Takemoto.M., Kawakami.B., Yamazaki.M., Watanabe.K.,
Kumagai.A., Itakura.S., Fukuzumi.Y., Fujimori.Y., Komiyama.M.,
Tashiro.H., Tanigami.A., Fujiwara.T., Ono.T., Yamada.K., Fujii.Y.,
Ozaki.K., Hirao.M., Ohmori.Y., Kawabata.A., Hikiji.T., Kobatake.N.,
Inagaki.H., Ikeda.Y., Okamoto.S., Okitani.R., Kawakami.T.,
Naguchi.S., Itoh.T., Shigeta.K., Senba.T., Matsumura.K.,
Nakajima.Y., Mizuno.T., Morinaga.M., Sasaki.M., Togashi.T.,
Oyama.M., Hata.H., Watanabe.M., Komatsu.T., Mizushima-Sugano.J.,
Satoh.T., Shirai.Y., Takahashi.Y., Nakagawa.K., Okumura.K.,
Nagase.T., Nomura.N., Kikuchi.H., Masuho.Y., Yamashita.R.,
Nakai.K., Yada.T., Nakamura.Y., Ohara.O., Isogai.T. and Sugano.S.
TITLE Complete sequencing and characterization of 21,243 full-length
human cDNAs

Nat. Genet. 36 (1), 40-45 (2004)
14702039
2
Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura.Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima.A., Sugiyama.A., Kawakami.B., Suzuki,Y., Sugano.S.,
Nagahari,K., Masuho.Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 1871)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(S-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES Location/Qualifiers
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Query Match 30.3%; Score 99; DB 8; Length 1871;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 229 CATGCTTTTCACCTCCACTGCATCTCTCGCTGCTCAAAACACGACGAGGTGTGCCATTG 288
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QY 289 GACACACAGAGTGGGAATTCCTCAAAAGTATGGGCACCTAG 327
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Job time : 2416 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 15:18:35 ; Search time 659.377 Seconds
(without alignments)
4100.974 Million cell updates/sec

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Perfect score: 327
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Scoring table: IDENTITY NUC
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Searched: 9793542 seqs, 413469005 residues
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Listing first 45 summaries

Database : Published Applications NA_Main:
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3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	327	100.0	453	7	US-10-242-535A-35025
4	327	100.0	453	7	US-10-085-783A-35025
5	327	100.0	467	7	US-10-242-535A-39933
6	327	100.0	467	7	US-10-085-783A-39933
7	327	100.0	471	7	US-10-242-535A-57254
8	327	100.0	471	7	US-10-085-783A-57254
9	327	100.0	472	7	US-10-242-535A-56068
10	327	100.0	472	7	US-10-085-783A-56068
11	327	100.0	508	8	US-10-085-783A-46292
12	327	100.0	523	7	US-10-242-535A-46292
13	327	100.0	523	7	US-10-085-783A-46292
14	325	99.4	476	3	US-09-918-995-17191
c 15	321.8	98.4	4543	5	US-10-198-846-11311
16	316	96.6	430	7	US-10-242-535A-54751
17	316	96.6	430	7	US-10-085-783A-54751
c 18	308.8	94.4	4476	8	US-10-357-930-25604
19	302.4	92.5	380	3	US-09-960-352-4677
c 20	301.2	92.1	5347	6	US-10-240-965-99
c 21	296.8	90.8	3484	8	US-10-723-860-1383
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c 23	296.8	90.8	5111	5	US-10-205-823-382

ALIGNMENTS

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US-10-242-535A-43377
; Sequence 43377, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 43377
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-43377

Query Match 100.0%; Score 327; DB 7; Length 433;
Best Local Similarity 100.0%; Pred. No. 5.4e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCGCGCAGCATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG	60
Db	20	ATGCGCGCAGCATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG	79
Qy	61	CGCTTTCAAGTGAAGAGTGAATGAGTATGATCTTTGGGCTGGGATATTGTTGAT	120
Db	80	CGCTTTGAAGTGAAGAGTGAATGAGTATGATCTTTGGGCTGGGATATTGTTGAT	139
Qy	121	AACGTGTCATCTCAGGAACCAATATGATCTTTGCATAGATGTCAAGCTAACACAG	180
Db	140	AACGTGTCATCTCAGGAACCAATATGATCTTTGCATAGATGTCAAGCTAACACAG	199
Qy	181	GGGTCCGCTACTTTCAGAAAGAGTGTCTGTCGATGGGAGTCTGTAAACCATGCTTTTTCAC	240
Db	200	GGGTCCGCTACTTTCAGAAAGAGTGTCTGTCGATGGGAGTCTGTAAACCATGCTTTTTCAC	259

	Qy	Db	Qy	Db
241	TTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTC	TTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTC	TTGGGAATTC	TTGGGAATTC
260	TTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTC	TTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTC	TTGGGAATTC	TTGGGAATTC
301	TTGGGAATTC	TTGGGAATTC	TTGGGAATTC	TTGGGAATTC
320	TTGGGAATTC	TTGGGAATTC	TTGGGAATTC	TTGGGAATTC
346	TTGGGAATTC	TTGGGAATTC	TTGGGAATTC	TTGGGAATTC
300	TTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTC	TTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTC	TTGGGAATTC	TTGGGAATTC
319	TTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTC	TTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTC	TTGGGAATTC	TTGGGAATTC

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RESULT 2
US-10-085-783A-43377
; Sequence 43377, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43377
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-43377

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Query Match	100.0%	Score 327;	DB 7;	Length 433;
Best Local Similarity	100.0%;	Prod. No. 5.4e-104;		
Matches 327;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCGCGCAGCGATGTGGATATCCCGAGCGCCAAACAGCGCGCGCGCAAGAAG	60	
Db	20	ATGCGCGCAGCGATGTGGATATCCCGAGCGCCAAACAGCGCGCGCGCAGAGAG	79	
QY	61	CGCTTTTGAAGTGA AAAAGTGGAAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGTTGAT	120	
Db	80	CGCTTTTGAAGTGA AAAAGTGGAAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGTTGAT	139	
QY	121	AACGTGTGCATCTGCAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTTAACCAAG	180	
Db	140	AACGTGTGCATCTGCAGGAACCAATTATGGATCTTTGCATAGAAATGTCAAGCTTAACCAAG	199	
QY	181	GCGTCCGCTACTTCAGAAAGTGTA CTGTCGCATGGGGAGTCTGTAAACCATGCTTTTTCAC	240	
Db	200	GCGTCCGCTACTTCAGAAAGTGTA CTGTCGCATGGGGAGTCTGTAAACCATGCTTTTTCAC	259	
QY	241	TTCCACTGCATCTCTCGCTGGCTCAAAAACAGCACAGGTGTGTGCCATTGGCAACACAGAGAG	300	
Db	260	TTCCACTGCATCTCTCGCTGGCTCAAAAACAGCACAGGTGTGTGCCATTGGCAACACAGAGAG	319	
QY	301	TGGGAATTC AAAAGTATGGGCACCTAG	327	
Db	320	TGGGAATTC AAAAGTATGGGCACCTAG	346	

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RESULT 3
US-10-242-535A-35025
; Sequence 35025, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005

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; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35025
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-35025

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Query Match	100.0%;	Score 327;	DB 7;	Length 453;
Best Local Similarity	100.0%;	Pred. No. 5.5e-104;		
Matches 327;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGGCGCAGCATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAACAAG	60	
Db				
Db	24	ATGGCGCAGCATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAACAAG	83	
Qy	61	CGCTTTGAAGTGAAGTGAAGTGCAGTAGCCCTCTGGCCCTGGGATATTGTGGTTGAT	120	
Db				
Db	84	CGCTTTGAAGTGAAGTGAAGTGCAGTAGCCCTCTGGCCCTGGGATATTGTGGTTGAT	143	
Qy	121	AACGTGCGCATCTGCAGGAACCAATTATGGATCTTTGCATAGAACTCAAGCTAACCAAG	180	
Db				
Db	144	AACGTGCGCATCTGCAGGAACCAATTATGGATCTTTGCATAGAACTCAAGCTAACCAAG	203	
Qy	181	CGGTCCGCTACTTCAGNAGAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTCAC	240	
Db				
Db	204	CGGTCCGCTACTTCAGNAGAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTCAC	263	
Qy	241	TTCCACTGCAATCTCTCGCTCGGCTCAAAAACAGCAGGTGTCTCCATTGGACAAACAGAGAG	300	
Db				
Db	264	TTCCACTGCAATCTCTCGCTCGGCTCAAAAACAGCAGGTGTCTCCATTGGACAAACAGAGAG	323	
Qy	301	TGGGAATTCAAAAGTATGGGCATAG	327	
Db				
Db	324	TGGGAATTCAAAAGTATGGGCATAG	350	

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RESULT 4
US-10-085-783A-35025
; Sequence 35025, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35025
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-35025
Query Match      100.0%   Score 327;   DB 7;   Length 453;

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; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-57254

Query Match      100.0%; Score 327; DB 7; Length 471;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
DB 17 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 76
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
DB 77 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 136
QY 121 AACTGTGCCATCTGCAGGAACCAACATTTGATGATCTTTGATAGAAATGCTCAAGCTAACCCAG 180
DB 137 AACTGTGCCATCTGCAGGAACCAACATTTGATGATCTTTGATAGAAATGCTCAAGCTAACCCAG 196
QY 181 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGCATGGGAGTGTGTAAACCATGCTTTTCAC 240
DB 197 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGCATGGGAGTGTGTAAACCATGCTTTTCAC 256
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAGAG 300
DB 257 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAGAG 316
QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
DB 317 TGGGAATTCAAAAGTATGGGCACTAG 343

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RESULT 8
US-10-085-783A-57254
; Sequence 57254, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
; US-10-085-783A-57254

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Query Match      100.0%; Score 327; DB 7; Length 471;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
DB 17 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 76
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
DB 77 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 136
QY 121 AACTGTGCCATCTGCAGGAACCAACATTTGATGATCTTTGATAGAAATGCTCAAGCTAACCCAG 180
DB 137 AACTGTGCCATCTGCAGGAACCAACATTTGATGATCTTTGATAGAAATGCTCAAGCTAACCCAG 196
QY 181 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGCATGGGAGTGTGTAAACCATGCTTTTCAC 240
DB 197 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGCATGGGAGTGTGTAAACCATGCTTTTCAC 256
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAGAG 300
DB 257 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAGAG 316
QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
DB 317 TGGGAATTCAAAAGTATGGGCACTAG 343

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RESULT 9
US-10-242-535A-56068
; Sequence 56068, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56068
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-242-535A-56068

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Query Match      100.0%; Score 327; DB 7; Length 472;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
DB 20 ATGGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120

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Db 80 CGCTTTGAAGTGAAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 139
Qy 121 AACTGTGCGCATCTGCAGGAACACACATTATGGATCTTTTCATAGATATGTCAGCTAACCG 180
Db 140 AACTGTGCGCATCTGCAGGAACACACATTATGGATCTTTTCATAGATATGTCAGCTAACCG 199
Qy 181 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 200 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 259
Qy 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAAACAGAGAG 300
Db 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAAACAGAGAG 319
Qy 301 TGGGAATTCCAAAGTATGGGCACTAG 327
Db 320 TGGGAATTCCAAAGTATGGGCACTAG 346

RESULT 10

US-10-085-783A-56068
; Sequence 56068, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56068
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-56068

Query Match 100.0%; Score 327; DB 7; Length 472;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGCGAGTGATGGATACCCGAGCGGCACCAACAGCGGCGGGCAAGAG 60
Db 20 ATGGCGGCGAGTGATGGATACCCGAGCGGCACCAACAGCGGCGGGCAAGAG 79
Qy 61 CGCTTTGAAGTGAAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 120
Db 80 CGCTTTGAAGTGAAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 139
Qy 121 AACTGTGCCATCTGCAGGAACACACATTATGGATCTTTGCATAGATATGTCAGCTAACCG 180
Db 140 AACTGTGCCATCTGCAGGAACACACATTATGGATCTTTGCATAGATATGTCAGCTAACCG 199
Qy 181 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 200 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 259

Qy 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAAACAGAGAG 300
Db 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAAACAGAGAG 319
Qy 301 TGGGAATTCCAAAGTATGGGCACTAG 327
Db 320 TGGGAATTCCAAAGTATGGGCACTAG 346

RESULT 11

US-10-913-937-3
; Sequence 3, Application US/10913937
; Publication No. US20050019813A1
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/10/913,937
; CURRENT FILING DATE: 2004-08-05
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(333)
; OTHER INFORMATION: Rbx1
US-10-913-937-3

Query Match 100.0%; Score 327; DB 8; Length 508;
Best Local Similarity 100.0%; Pred. No. 5.8e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGGCGAGTGATGGATACCCGAGCGGCACCAACAGCGGCGGGCAAGAG 60
Db 7 ATGGCGGCGAGTGATGGATACCCGAGCGGCACCAACAGCGGCGGGCAAGAG 66
Qy 61 CGCTTTGAAGTGAAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 120
Db 67 CGCTTTGAAGTGAAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 126
Qy 121 AACTGTGCCATCTGCAGGAACACACATTATGGATCTTTGCATAGATATGTCAGCTAACCG 180
Db 127 AACTGTGCCATCTGCAGGAACACACATTATGGATCTTTGCATAGATATGTCAGCTAACCG 186
Qy 181 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 187 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
Qy 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAAACAGAGAG 300
Db 247 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAAACAGAGAG 306
Qy 301 TGGGAATTCCAAAGTATGGGCACTAG 327
Db 307 TGGGAATTCCAAAGTATGGGCACTAG 333

RESULT 12

US-10-242-535A-46292
; Sequence 46292, Application US/10242535A

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; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46292
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-46292

Query Match      100.0%; Score 327; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 5.9e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAG 60
Db 19 ATGGCGGCGAGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAG 78
QY 61 CGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGAT 120
Db 79 CGCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGAT 138
QY 121 AACTGTGCCATCTGCAGGAACCAATATGGATCTTTGCATAGAATGTCAAGCTAACCCAG 180
Db 139 AACTGTGCCATCTGCAGGAACCAATATGGATCTTTGCATAGAATGTCAAGCTAACCCAG 198
QY 181 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 199 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 258
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACAGCAGGTGTGTCATTGGACAAACAGAGAG 300
Db 259 TTCCACTGCATCTCTCGCTGGCTCAAAACAGCAGGTGTGTCATTGGACAAACAGAGAG 318
QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
Db 319 TGGGAATTCAAAAGTATGGGCACTAG 345

RESULT 14
US-09-918-995-17191
; Sequence 17191, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17191
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-17191

Query Match      99.4%; Score 325; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.9e-103;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGCGGCGAGCGATGGATGATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAGCG 62
Db 74 GCGCGGCGAGCGATGGATGATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAGCG 133
QY 63 CTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGATAA 122
Db 134 CTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGGTTGATAA 193
QY 123 CTGTGCCATCTGCAGGAACCAATATGGATCTTTGCATAGAATGTCAAGCTAACCCAGGC 182

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Search completed: March 8, 2006, 17:28:04
Job time : 661.377 secs

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3	172.4	52.9	438	9	US-11-096-568A-28569	
4	169.8	51.7	342	9	US-11-096-568A-14405	
5	130	39.8	366	7	US-10-932-182A-2279	
6	130	39.8	366	7	US-10-932-182A-2279	
7	123.6	37.8	366	7	US-10-932-182A-2279	
8	123.6	37.8	366	7	US-10-932-182A-78459	
9	76	23.2	342	8	US-10-932-182A-78459	
c	10	74	22.6	153	7	US-10-821-234-554
c	11	74	22.6	153	7	US-10-932-182A-81177
12	68.2	20.9	546	12	US-11-128-061-5740	
13	68.2	20.9	546	12	US-11-128-049-5740	
14	68.2	20.9	579	12	US-11-128-061-2098	
15	68.2	20.9	579	12	US-11-128-049-2098	
c	16	65.4	20.0	207	7	US-10-932-182A-6146
c	17	65.4	20.0	207	7	US-10-932-182A-6146
c	18	42.8	13.1	450	9	US-11-057-484A-14
19	39.6	12.1	3404	12	US-11-045-468A-18	
20	34.2	10.5	201	8	US-10-995-561-20992	
					Sequence 11809, A	
					Sequence 26820, A	
					Sequence 28569, A	
					Sequence 14405, A	
					Sequence 2279, A	
					Sequence 2279, A	
					Sequence 78459, A	
					Sequence 78459, A	
					Sequence 554, App	
					Sequence 81177, A	
					Sequence 81177, A	
					Sequence 5740, App	
					Sequence 5740, App	
					Sequence 2098, App	
					Sequence 2098, App	
					Sequence 6146, App	
					Sequence 6146, App	
					Sequence 14, Appl	
					Sequence 18, Appl	
					Sequence 20992, A	

Query Match	54.2%;	Score 177.2;	DB 9;	Length 660;
Best Local Similarity	78.5%;	Pred. No. 3.2e-46;		
Matches 212;	Conservative 0;	Mismatches 58;	Indels 0;	Gaps 0;
58	AAGCGCTTTGAAGTCAAAAAGTGGAAATGACAGTAGCCCTCTGGCGCTGGGATATTGTGGTT	117		
193	AAGCGCTTCGAGATCAAGAAGTGGAAAGCGCGTCGCGCTCTGGCGTGGGACATCGTGGTG	252		
118	GATAACTGTGCCATCTGCAGGAAACCAATTATGGATCTTTTGCATAGANATGTCGAAGCTAAC	177		
253	GACAACCTGGCCATCTGCCGTAAACCAATCATGGATTTATGCATCGAGTCCGAGGCCAAC	312		
178	CAGGCGTCCGCTACTCTCAAGAGAGTGATCTGTCGATGGGAGTCTGTAAACCATGCTTTT	237		
313	CAGGCCAGGCCACCAGCGAGGAGTGCACCGTCGATGGGTGTCGTGTAATCATGCTTTC	372		
238	CACTTCCACTGCATCTCTCGCTGGCTCAAAAACACGACAGGTGTGTCCATTGGACAAACAGA	297		
373	CACTTCCACTGCATCAGCAGGTGGCTCAAGACTCGCCAAAGTGTGCCCACTAGACAACAGC	432		
298	GAGTGGGAATTCCAAAGATTATGGGCACTAG	327		


```
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78459
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-78459

Query Match      37.8%; Score 123.6; DB 7; Length 366;
Best Local Similarity 66.5%; Pred. No. 2.8e-29;
Matches 177; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 55 AAGAAGCGCTTTCAAGTGAAGTGAATGCAAGTACGCTCTGGGCGCTGGGATATTGTG 114
    |||||
Db 94 AAGAAGAGATTTGAAATTAAGAAATGACCCGAGTGGCTTTTGGTCAATGGGATATAGCT 153
    |||||
QY 115 GTTGATAACTGTGCCATCTGCAGAACCAACATATGATCTTTTGCATAGAACTCAAGCT 174
    |||||
Db 154 GTTGACAACCTGTCTATTTCAGGAACCAATATAATGGAACCATGCAATGAATGCCAGCCA 213
    |||||
QY 175 AACGAGCGCTCCGCTACTTCCAGAAAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCT 234
    |||||
Db 214 AAGCCATGACGACACTGATATGATGTGTAGCAGCGCTGGGTGCTGTATATACGCT 273
    |||||
QY 235 TTTCACCTCCATGTCATCTCTCGCTGCTCAAAACAGACAGAGTGTGTCATTGGCAAC 294
    |||||
Db 274 TTCCATTGCACTGTATTATAAATGATCAAGACAAGACAGCATGCCCATTTAGATAAC 333
    |||||
QY 295 AGAGAGTGGGAATTCAAAGTATGG 320
    |||||
Db 334 CAACCTTGGCAGTTAGCAAGATCGG 359
    |||||

RESULT 9
US-10-821-234-554
; Sequence 554, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 554
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-554

Query Match      23.2%; Score 76; DB 8; Length 342;
Best Local Similarity 56.9%; Pred. No. 3.5e-14;
Matches 164; Conservative 0; Mismatches 115; Indels 9; Gaps 1;

QY 26 CCCGAGCGGCCACCAACAGCGCGCGCGGCAAGAGCGCTTTGAAAGTGAAGGAAAGTGAATG 85
    |||||
Db 50 CCGGAGCTCAGGCTCCCAAGTCCGAGGCGGACAGAGATGTTCTCCCTCAAGAAGTGAACG 109
    |||||
QY 86 CAGTAGCCCTCTGGCCCTGGGATATTGTGTTGATACTGTGCCATCTGCAGGAACCAACA 145
    |||||
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Db 110 CGGTGCCCATGTGGAGCTGGAGCTGGAGTGCAGTACGCTGCGCATCTGCAGGTCAGG 169
    |||||
QY 146 TTATGATCTTTGCATAGATGTCAAGCTAACACGCGCTCCGCTACTTTCAGAGAGTGA 205
    |||||
Db 170 TGATGATCCCTGTCTTAGATGTCAAGCTGAAAA-----CAAAACAAGAGACTGTG 220
    |||||
QY 206 CTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCACTTCACATGCACTCTCTCGCTGGCTCA 265
    |||||
Db 221 TTGTGCTCTGGGAGAAATGTAATCATCTTCCACAACTGCTGCAATGTCCTGTGGGTGA 280
    |||||
QY 266 AAACACGACAGGTGTCTCAATTGGCAACACAGAGAGTGGGAATTCAAA 313
    |||||
Db 281 AACAGAACAAATCGCTGCCCTCTCTGCCAGCAGACTGGGTGGTCCAAA 328
    |||||

RESULT 10
US-10-932-182A-81177/c
; Sequence 81177, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81177
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-81177

Query Match      22.8%; Score 74; DB 7; Length 153;
Best Local Similarity 75.4%; Pred. No. 1.2e-13;
Matches 92; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 55 AAGAAGCGCTTTGAAGTGAAGTGAATGCAAGTACGCTCTGGGCGCTGGGATATTGTG 114
    |||||
Db 128 AAGAAGAGATTTGAAATTAAGAAATGACCGCAGTGGCTTTTGGTCAATGGGATATAGCT 69
    |||||
QY 115 GTTGATAACTGTGCCATCTGCAGGAACCAACATATGATCTTTGCAATAGAAATGTCAAGCT 174
    |||||
Db 68 GTTGACAACCTGTCTATTTCAGGAACCAATATAATGGAACCATGCAATGAATGCCAGCCA 9
    |||||
QY 175 AA 176
    ||
Db 8 AA 7

RESULT 11
US-10-932-182A-81177/c
; Sequence 81177, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81177
; LENGTH: 153
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US-11-128-061-2098
; Sequence 2098, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.

```


Result No.	Query			Length	DB	ID	Description
	Score	Match					
1	327	100.0	482	3	US-09-5113-999C-3894		Sequence 3894, Ap
2	327	100.0	507	3	US-09-949-016-4940		Sequence 4940, Ap
3	327	100.0	508	3	US-09-914-324A-3		Sequence 3, Appli
4	290.2	88.7	504	3	US-09-914-324A-5		Sequence 5, Appli
5	253.6	77.6	3208	3	US-09-780-016-27		Sequence 27, Appl
6	253.6	77.6	3208	3	US-10-214-811-27		Sequence 27, Appl
7	253.6	77.6	3208	3	US-10-766-074-27		Sequence 27, Appl
8	170	52.0	402	3	US-09-5113-999C-10371		Sequence 10371, A
9	170	52.0	463	3	US-09-621-976-15180		Sequence 15180, A
10	153.2	46.9	411	3	US-09-640-211A-1731		Sequence 1731, Ap
C 11	138.2	42.3	490	3	US-09-270-767-26812		Sequence 26812, A
C 12	138.2	42.3	1101	3	US-09-270-767-11265		Sequence 11265, A
13	123.6	37.8	480	3	US-09-914-324A-4		Sequence 4, Appli
14	114.4	35.0	357	3	US-09-248-796A-5495		Sequence 5495, Ap
15	92.6	28.3	25274	3	US-09-949-016-16682		Sequence 16682, A
16	90	27.5	301	3	US-09-313-294A-492		Sequence 492, App
17	74	22.6	342	3	US-09-826-312A-7		Sequence 7, Appli
18	74	22.6	342	3	US-09-542-497A-7		Sequence 7, Appli
19	74	22.6	342	3	US-10-108-767-7		Sequence 7, Appli
20	46.4	14.2	439	3	US-09-799-451-296		Sequence 296, App
21	36	11.0	601	3	US-09-949-016-174803		Sequence 174803, A
22	33.6	10.3	87734	3	US-09-949-016-17521		Sequence 17521, A
C 23	33.4	10.2	170	3	US-09-270-767-26253		Sequence 26253, A
C 24	33.4	10.2	585	3	US-09-270-767-10788		Sequence 10788, A


```
RESULT 7
US-10-766-074-27
; Sequence 27, Application US/10766074
; Patent No. 6881563
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn.
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/10/766,074
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/10/214,811
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-074-27

Query Match 77.6%; Score 253.6; DB 3; Length 3208;
Best Local Similarity 98.5%; Pred. No. 2.6e-77; Indels 0; Gaps 0;
Matches 256; Conservative 0; Mismatches 4;

QY 68 AAGTGAAGTGAATGCAGTAGTCCCTCTGGGCGCTGGGATATTGTGGTTGATACTGTG 127
DB 2765 AAAAAAATGAAATGCAGTAGTCCCTCTGGGCGCTGGGATATTGTGGTTGATACTGTG 2824

QY 128 CACTCTGCAGGACCACTATGATCTTTGGCATAGATGTCAAGCTAACCGCGCTCCG 187
DB 2825 CCATCTGCAGGACCACTATGATCTTTGGCATAGATGTCAAGCTAACCGCGCTCCG 2884

QY 188 CTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTCACTTCCACT 247
DB 2885 CTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTCACTTCCACT 2944

QY 248 GCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACACAGAGTGGGAAT 307
DB 2945 GCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACACAGAGTGGGAAT 3004

QY 308 TCCAAAAGTATGGCACTAG 327
DB 3005 TCCAAAAGTATGGCACTAG 3024

RESULT 8
US-09-513-999C-10371
; Sequence 10371, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2,REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
```

```
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10371
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 20
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 38
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 79
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-10371

Query Match 52.0%; Score 170; DB 3; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e-48; Indels 0; Gaps 0;
Matches 170; Conservative 0; Mismatches 0;

QY 158 GCATAGAATGTCAAGCTAACCGAGGTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGG 217
DB 106 GCATAGAATGTCAAGCTAACCGAGGTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGG 165

QY 218 GAGTCTGTAAACCATGCTTTTTCACCTTCCACTGTCATCTCTCGTGGCTCAAAACACGACAGG 277
DB 166 GAGTCTGTAAACCATGCTTTTTCACCTTCCACTGTCATCTCTCGTGGCTCAAAACACGACAGG 225

QY 278 TGTGTCCTTGGACACAGAGTGGGAATTCAAAAGTATGGGCACTAG 327
DB 226 TGTGTCCTTGGACACAGAGTGGGAATTCAAAAGTATGGGCACTAG 275

RESULT 9
US-09-621-976-15180
; Sequence 15180, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15180
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 74
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-15180

Query Match 52.0%; Score 170; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.1e-48; Indels 0; Gaps 0;
Matches 170; Conservative 0; Mismatches 0;

QY 158 GCATAGAATGTCAAGCTAACCGAGGTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGG 217
DB 101 GCATAGAATGTCAAGCTAACCGAGGTCCGCTACTTTCAGAAAGTGTACTGTGCGCATGGG 160

QY 218 GAGTCTGTAAACCATGCTTTTTCACCTTCCACTGTCATCTCTCGTGGCTCAAAACACGACAGG 277
DB 161 GAGTCTGTAAACCATGCTTTTTCACCTTCCACTGTCATCTCTCGTGGCTCAAAACACGACAGG 220
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RESULT 11
US-09-270-767-26812/c
; Sequence 26812, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26812
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26812

Query Match          42.3%; Score 138.2; DB 3; Length 490;
Best Local Similarity 71.0%; Pred. No. 1.2e-37;
Matches 198; Conservative 0; Mismatches 78; Indels 3; Gaps 1

```

Query Match	42.3%;	Score 138.2;	DB 3;	Length 1101;
Best Local Similarity	71.0%;	Pred. No. 1.9e-37;		
Matches 198;	Conservative	0;	Mismatches 78;	Indels 3; Gaps 1;
Qy	49	GCGGCGAAGAAGCGCTTTTGAAGTGA AAAAGTGGAAATGCAGTAGCCCTCTGGGCGCTGGGAT	108	
Db	933	GCCAGGACGGAGCGCTTTGTGGTGAAGAAATGGTTGGCGACGCCATGTGGGATGGGAC	874	
Qy	109	ATTGTGGTTGATAACTGTGCCATCTCCAGAAACCAATTATGATCTTTTGCATAGATGT	168	
Db	873	GTAGCAGTGACAACTGTGCGCATCTGCCGTAAACCATCATGAACCTGTGCATCGAGTGC	814	
Qy	169	CAAGCTTAACCAGCGCTCCGCTACTTTCAGAAAGAGTGACTGTGCGCATGGGAGTGCTGTAAAC	228	
Db	813	CAGCGGACCC--CGAATGCAAAACCAAGACGAGTGACACTGTGTGCTTTGGGCGGAGTGCAAC	757	
Qy	229	CATGCTTTTCACCTTCCATGTCATCTCTCGCTGCGCTCAAAAACAGCAGGTGTCTCCATTG	288	
Db	756	CAGCGATTCATTACCACTGTCATCGGCGCGCTGGTTGAAAACGCGCTGGTCTGTCCGCTG	697	
Qy	289	GACAAACAGAGTGGGAAATTCAAAAAGTAGTGGGCACTAG	327	
Db	696	GACAAACAGAGTGGGCTTACACAGAGTAGTCGGCCGCTAG	658	

RESULT 13
US-09-914-324A-4
; Sequence 4, Application US/09914324A
; Patent No. 6958709
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi

```

; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: No. 6858709e1 Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(369)
; OTHER INFORMATION: Rbx1
; US-09-914-324A-4

```

	Query Match	37.8%	Score 123.6	DB 3	Length 480
	Best Local Similarity	66.5%	Pred. No. 1.4e-32		
	Matches 177	Conservative 0	Mismatches 89	Indels 0	Gaps 0
Qy	55	AAGAAGCGCTTTTGAAGTCGAAAAAGTGGAAATGCAGTAGCCCTCTCGGCGCTGGGATATTG	114		
Db	97	AAGNAGAGATTTTGAATTTAAGAAATGACCGCAGTGGCGTTTTTGGTCATGGGATATAGCT	156		
Qy	115	GTTGATAACTGTGGCACTCTGCAGAACACACATTATGGATCTTTGCATAGAATGTCACAACT	174		
Db	157	GTTGACAACTGTGCTATTGTCAGGAACCATATAATGGAACCATGCAATTTGAATGCCAGCCA	216		
Qy	175	AACCAGGCGTCGCGTACTTTCAGAAAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCT	234		
Db	217	AAGCCATGACGGACACTGATAATGATGTGTAGCAGCCTGGGGTGTCTGTAATCACGCT	276		
Qy	235	TTTCACCTCCACTGCACTCTCGCTGGCTCAAAACACACAGGCTGTGTCATTGGACAAAC	294		
Db	277	TTTCATTGCACTGTATTAAATGGAATCAAGACACAGAGAGCGCATGCCCATTAGATATAC	336		
Qy	295	AGAGAGTGGGAATTTCCAAAAGTATGG	320		
Db	337	CAACCTTTGGCAGTTTAGCAAGATCGG	362		

RESULT 14
 US-09-248-796A-5495
 ; Sequence 5495, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstein et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 5495
 ; LENGTH: 357
 ; TYPE: DNA
 ; ORGANISM: Candida albicans
 ; US-09-248-796A-5495

Query Match 35.0%; Score 114.4; DB 3; Length 357;
Best Local Similarity 66.8%; Pred. No. 1.9e-29;
Matches 179; Conservative 0; Mismatches 86; Indels 3; Gaps 1;

Qy	62	CTTTGAAGTCAAAAGTGAATGCAGCTAGCCCTCTGGCCCTGGGATATGTTGGTTTGATA	121
Db	89	GATTTGAAGTCAAAAGTGAATGCAGCTAGCCCTCTGGCCCTGGGATATGCAAAATTGAAA	148
Qy	122	ACTGTGCATCTGCAGGAACACACATTATGGATCTTTGCATAGAATGTCAAGCTAA--CC	178
Db	149	ATTGTGCCATTTGTAGAAATCATTTAATGGAACCATGTATTGAATGTCAACCAAAATGCTA	208
Qy	179	AGGCGTCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGGAGTCTGTAACCATGCTTTTC	238
Db	209	TGGGTAATATATTCCTTCAGAAAGTGTATTCCTGCTTGGGGAGTATGTAATCATGCAATTC	268
Qy	239	ACTTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGTGTGTCCATTGGGACAAACAGAG	298
Db	269	ATTTACATTTGTTAGAAAGTGGTTGAANAACAGAAATGCATGTCCTCTGGATAGTACTA	328
Qy	299	AGTGGGAATCCAAAGATATGGGCACTA	326
Db	329	ATTGGACTTATCAAAAATTGGGTAAATTA	356

```

RESULT 15
US-09-949-016-16682
; Sequence 16682, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16682.
; LENGTH: 25274
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16682

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	Query Match	28.3%	Score 92.6	DB 3	Length 25274
	Best Local Similarity	96.0%	Pred. No. 6.1e-21		
	Matches 95	Conservative 0	Mismatches 4	Indels 0	Gaps 0
Qy	221	TCGTAAACATGCTTTTCACTTCCACTGCACTCTCGCTGGCTCAAAACACGACAGGTGT	280		
Db	18403	TCCTTCAGCATGCTTTTCACTTCCACTGCACTCTCGCTGGCTCAAAACACGACAGGTGT	18462		
Qy	281	GTCCATTGGACAACAGAGAGTGGGAATTCAAAAGTATG	319		
pb	18463	GTCCATTGGACAACAGAGAGTGGGAATTCAAAAGTAGG	18501		

Search completed: March 8, 2006, 14:48:17
Job time : 100.735 secs